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TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND METHODS OF MAKING AND USING SAME

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit under 35 U.S.C. 119(e) of provisional applications U.S. Serial No. 60/404,356, filed August 16, 2002; U.S. Serial No. 60/479,432, filed June 18, 2003; and Attorney Docket No. 3554.096, filed July 31, 2003; the contents of each of which are expressly incorporated herein by reference in their entirety.

[0002] This application is a continuation-in-part of copending U.S. Serial No. 10/195,908, filed July 15, 2002; which is a continuation-in-part of U.S. Serial No. 09/437,277, filed November 11, 1999, now U.S. Patent No. 6,444,447, issued September 3, 2002; which claims benefit under 35 U.S.C. 119(e) of U.S. Provisional No. 60/107,929, filed November 11, 1998, the contents of both of which are expressly incorporated herein in their entirety by reference.

[0003] Said U.S. Serial No. 10/195,908 is also a continuation-in-part of U.S. Serial No. 09/283,402, filed April 1, 1999, now abandoned; which claims benefit under 35 U.S.C. 119(e) of U.S. Provisional No. 60/080,414, filed April 2, 1998, the contents of both of which are expressly incorporated herein in their entirety by reference.

[0004] Said U.S. Serial No. 10/195,908 is also a continuation-in-part of copending U.S. Serial No. 09/842,484, filed April 25, 2001; which claims benefit under 35 U.S.C. 119(e) of U.S. Provisional No. 60/199,538, filed April 25, 2000, the contents of both of which are expressly incorporated herein in their entirety by reference.

[0005] Said U.S. Serial No. 10/195,908 is also a continuation-in-part of copending U.S. Serial No. 10/142,143, filed May 8, 2002; which claims benefit under 35 U.S.C. 119(e) of U.S. Provisional No. 60/289,554, filed May 8, 2001, the contents of both of which are expressly incorporated herein in their entirety by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0006] This application was supported in part by National Research Grant C2163601 from the National Science Foundation. The United States Government may have rights in and to this application by virtue of this funding.

BACKGROUND

[0007] Field of the Invention

[0008] The present invention relates to methodology for the production of polymers, such as polysachharides or oligosaccharides, by a glycosaminoglycan synthase and, more particularly, polymer production utilizing glycosaminoglycan synthases from *Pasteurella multocida*.

[0009] Various glycosaminoglycans show potential as non-toxic therapeutic agents to modulate blood coagulation, cancer metastasis, or cell growth. Complex sugars cause biological effects by binding to target proteins including enzymes and receptors. Methodologies to synthesize many compounds, however, and to test for potency and selectivity are limiting steps in drug discovery. Moreover, glycosaminoglycans of different sizes can have dramatically different biological effects. As such, the presently claimed and disclosed invention also relates to a chemoenzymatic synthesis methodology to create both pure, chimeric, and hybrid polymers composed of hyaluronan, chondroitin, keratan, dermatan, heparin units, and combinations thereof (e.g. "chimeric or hybrid" polymers), wherein the pure, chimeric and hybrid polymers are substantially monodisperse in size.

[00010] Description of the Related Art

[00011] Polysaccharides are large carbohydrate molecules comprising from about 25 sugar units to thousands of sugar units. Oligosaccharides are smaller carbohydrate molecules comprising less than about 25 sugar units. Animals, plants, fungi and bacteria produce an enormous variety of polysaccharide structures that are involved in numerous important biological functions such as structural elements, energy storage, and cellular interaction mediation. Often, the polysaccharide's biological function is due to the interaction of the polysaccharide with proteins such as receptors and growth factors. The glycosaminoglycan class of polysaccharides and oligosaccharides, which includes heparin, chondroitin, dermatan, keratan, and hyaluronic acid, plays major roles in determining cellular behavior (e.g. migration, adhesion) as well as the rate of cell proliferation in mammals. These polysaccharides and oligosaccharides are, therefore, essential for the correct formation and maintenance of the organs of the human body.

[00012] Several species of pathogenic bacteria and fungi also take advantage of the polysaccharide's role in cellular communication. These pathogenic microbes form polysaccharide surface coatings or capsules that are identical or chemically similar to host molecules. For instance, Group A & C *Streptococcus* and Type A *Pasteurella multocida* produce authentic hyaluronic acid capsules, and other *Pasteurella multocida* (Type F and D) and pathogenic *Escherichia coli* (K4 and K5) are known to make capsules composed of polymers very similar to chondroitin and heparin. The pathogenic microbes form the polysaccharide surface coatings or capsules because such a coating is nonimmunogenic and protects the bacteria from host defenses, thereby providing the equivalent of molecular camouflage.

[00013] Enzymes alternatively called synthases, synthetases, or transferases, catalyze the polymerization of polysaccharides found in living organisms. Many of the known enzymes also polymerize activated sugar nucleotides. The most prevalent sugar donors contain UDP, but ADP, GDP, and CMP are also used depending on (1) the particular sugar to be transferred and (2) the organism. Many types of polysaccharides are found at, or outside of, the cell surface. Accordingly, most of the synthase activity is typically associated with either the plasma membrane on the cell periphery or the Golgi apparatus membranes that are involved in secretion. In general, these membrane-bound synthase proteins are difficult to manipulate by typical procedures, and only a few enzymes have been identified after biochemical purification.

[00014] A larger number of synthases have been cloned and sequenced at the nucleotide level using "reverse genetic" approaches in which the gene or the complementary DNA (cDNA) was obtained before the protein was characterized. Despite this sequence information, the molecular details concerning the three-dimensional native structures, the active sites, and the mechanisms of catalytic action of the polysaccharide synthases, in general, are very limited or absent. For example, the catalytic mechanism for glycogen synthesis is not yet known in detail even though the enzyme was discovered decades ago. In another example, it is still a matter of debate whether most of the enzymes that produce heteropolysaccharides utilize one UDP-sugar binding site to transfer both precursors, or alternatively, if there exists two dedicated regions for each substrate.

[00015] A wide variety of polysaccharides are commercially harvested from many sources, such as xanthan from bacteria, carrageenans from seaweed, and gums from trees. This substantial industry supplies thousands of tons of these raw materials for a multitude of consumer products ranging from ice cream desserts to skin cream cosmetics. Vertebrate tissues and pathogenic bacteria are the sources of more exotic polysaccharides utilized in the medical field – e.g. as surgical aids, vaccines, and anticoagulants. For example, two glycosaminoglycan polysaccharides, heparin from pig intestinal mucosa and hyaluronic acid from rooster combs,

are employed in several applications including clot prevention and eye surgery, respectively. Polysaccharides extracted from bacterial capsules (e.g. various *Streptococcus pneumoniae* strains) are utilized to vaccinate both children and adults against disease with varying levels of success. However, for the most part, one must use the existing structures found in the raw materials as obtained from nature. In many of the older industrial processes, chemical modification (e.g. hydrolysis, sulfation, deacetylation) is used to alter the structure and properties of the native polysaccharide. However, the synthetic control and the reproducibility of large-scale reactions are not always successful. Additionally, such polysaccharides are only available having a large molecular weight distribution, and oligosaccharides of the same repeat units are not available.

[00016] Some of the current methods for designing and constructing carbohydrate polymers *in vitro* utilize: (i) difficult, multistep sugar chemistry, or (ii) reactions driven by transferase enzymes involved in biosynthesis, or (iii) reactions harnessing carbohydrate degrading enzymes catalyzing transglycosylation or hydrolysis. The latter two methods are often restricted by the specificity and the properties of the available naturally occurring enzymes. Many of these enzymes are neither particularly abundant nor stable but are almost always expensive. Overall, the procedures currently employed yield polymers containing between 2 and about 12 sugars. Unfortunately, many of the physical and biological properties of polysaccharides do not become apparent until the polymer contains 25, 100, or even thousands of monomers.

[00017] As stated above, polysaccharides are the most abundant biomaterials on earth, yet many of the molecular details of their biosynthesis and function are not clear. Hyaluronic acid or "HA" is a linear polysaccharide of the glycosaminoglycan class and is composed of up to thousands of β(1,4)GlcUA-β(1,3)GlcNAc repeats. In vertebrates, HA is a major structural element of the extracellular matrix and plays roles in adhesion and recognition. HA has a high negative charge density and numerous hydroxyl groups, therefore, the molecule assumes an extended and hydrated conformation in solution. The viscoelastic properties of cartilage and synovial fluid are, in part, the result of the physical properties of the HA polysaccharide. HA also interacts with proteins such as CD44, RHAMM, and fibrinogen thereby influencing many natural processes such as angiogenesis, cancer, cell motility, wound healing, and cell adhesion.

[00018] There are numerous medical applications of HA. For example, HA has been widely used as a viscoelastic replacement for the vitreous humor of the eye in ophthalmic surgery during implantation of intraocular lenses in cataract patients. HA injection directly into joints is also used to alleviate pain associated with arthritis. Chemically cross-linked gels and films are also utilized to prevent deleterious adhesions after abdominal surgery. Other researchers using other methods have demonstrated that adsorbed HA coatings also improve the

biocompatibility of medical devices such as catheters and sensors by reducing fouling and tissue abrasion.

[00019] HA is also made by certain microbes that cause disease in humans and animals. Some bacterial pathogens, namely Gram-negative *Pasteurella multocida* Type A and Gram-positive *Streptococcus* Group A and C, produce an extracellular HA capsule which protects the microbes from host defenses such as phagocytosis. Mutant bacteria that do not produce HA capsules are 10^2- and 10^3-fold less virulent in comparison to the encapsulated strains. Furthermore, the *Paramecium bursaria* Chlorella virus (PBCV-1) directs the algal host cells to produce a HA surface coating early in infection.

[00020] The various HA synthases ("HAS"), the enzymes that polymerize HA, utilize UDP-GlcUA and UDP-GlcNAc sugar nucleotide precursors in the presence of a divalent Mn, Mg, or Co ion to polymerize long chains of HA. The HA chains can be quite large ($n=10^2$ to 10^4). In particular, the HASs are membrane proteins localized to the lipid bilayer at the cell surface. During HA biosynthesis, the HA polymer is transported across the bilayer into the extracellular space. In all HASs, a single species of polypeptide catalyzes the transfer of two distinct sugars. In contrast, the vast majority of other known glycosyltransferases transfer only one monosaccharide.

[00021] HasA (or spHAS) from Group A *Streptococcus pyogenes* was the first HA synthase to be described at the molecular level. The various vertebrate homologs (*Xenopus* DG42 or XlHAS1; murine and human HAS1, HAS2, and HAS3) and the viral enzyme, A98R, are quite similar at the amino acid level to certain regions of the HasA polypeptide chain (~30% identity overall) and were discovered only after the sequence of spHAS was disclosed in 1994 . At least 7 short motifs (5-9 residues) interspersed throughout these Class I enzymes are identical or quite conserved. The evolutionary relationship among these HA synthases from such dissimilar sources is not clear at present. The enzymes are predicted to have a similar overall topology in the bilayer: membrane-associated regions at the amino and the carboxyl termini flank a large cytoplasmic central domain (~200 amino acids). The amino terminal region appears to contain two transmembrane segments, while the carboxyl terminal region appears to contain three to five membrane-associated or transmembrane segments, depending on the species. Very little of these HAS polypeptide chains are expected to be exposed to the outside of the cell.

[00022] With respect to the reaction pathway utilized by this group of enzymes, mixed findings have been reported from indirect experiments. The Group A streptococcal enzyme was reported to add sugars to the nonreducing terminus of the growing chain as determined by selective labeling and degradation studies. Using a similar approach, however, two laboratories working with the enzyme preparations from mammalian cells concluded that the new sugars

were added to the reducing end of the nascent chain. In comparing these various studies, the analysis of the enzymatically-released sugars from the streptococcal system added more rigorous support for their interpretation. In another type of experiment, HA made in mammalian cells was reported to have a covalently attached UDP group as measured by an incorporation of low amounts of radioactivity derived from ^{32}P-labeled UDP-sugar into an anionic polymer. This data implied that the last sugar was transferred to the reducing end of the polymer. Thus, it remains unclear if these rather similar HAS polypeptides from vertebrates and streptococci actually utilize different reaction pathways.

[00023] On the other hand, the Class II HAS, pmHAS, has many useful catalytic properties including the ability to elongate exogenous acceptors at the non-reducing end with HA chains. The homologous chondroitin synthase, pmCS, also is useful, but it adds chondroitin chains to the acceptor's non-reducing terminus.

[00024] To facilitate the development of biotechnological medical improvements, the present invention provides a method for the production of glycosaminoglycans of HA, chondroitin, and chimeric or hybrid molecules incorporating both HA and chondroitin, wherein the glycosaminoglycans are substantially monodisperse and thus have a defined size distribution.

[00025] The present invention also encompasses the use of one or more modified synthases that have the ability to produce non-natural polymers. An advantage of these mutant enzymes is that their altered specificity allows new useful groups or units to be added to the polymer.

[00026] The present invention also encompasses the methodology of polysaccharide or oligosaccharide polymer grafting, i.e. HA, heparosan or chondroitin, using either a hyaluronan synthase (pmHAS) or a chondroitin synthase (pmCS) or a heparin synthase (pmHS, also referred to as pmHS1, and PglA, also referred to as pmHS2), respectively, from various types of *P. multocida*. Modified versions of the pmHAS or pmCS or pmHS1, or pmHS2 enzymes (whether genetically or chemically modified) can also be utilized to graft on polysaccharides of various size and composition. Thus, the present invention results in (1) the targeting of specific, desirable size distributions or size ranges and (2) the synthesis of monodisperse (narrow size distribution) polymers.

SUMMARY OF THE INVENTION

[00027] A unique HA synthase, pmHAS, from the fowl cholera pathogen, Type *A P. multocida,* has been identified and cloned and is disclosed and claimed in co-pending U.S. Serial No. 10/217,613, filed August 12, 2002, and entitled "DNA Encoding Hyaluronan Synthase From Pasteurella Multocida and Methods," the contents of which are hereby expressly incorporated herein in their entirety. Expression of this single, 972-residue protein allows *Escherichia coli* host cells to produce HA capsules *in vivo*; normally *E. coli* does not make HA. Extracts of recombinant *E. coli*, when supplied with the appropriate UDP-sugars, make HA *in vitro*. Thus, the pmHAS is an authentic HA synthase.

[00028] A unique chondroitin synthase, pmCS, from Type F *P. multocida*, has been identified and cloned and is disclosed and claimed in co-pending U.S. Serial No. 09/842,484, filed April 25, 2002, and entitled "Chondroitin Synthase Gene and Methods of Making and Using Same", the contents of which are hereby expressly incorporated herein in their entirety. Expression of the catalytically active portion (residues 1-704) of this single, 965-residue protein allows *E. coli* host cells to produce an enzyme that will polymerize chondroitin chains. Laboratory strains of *E. coli* normally do not make chondroitin. Extracts of recombinant *E. coli*, when supplied with the appropriate UDP-sugars, make chondroitin *in vitro*. Thus, the pmCS is an authentic chondroitin synthase.

[00029] Two unique heparin synthases, PglA (now referred to as pmHS2) and pmHS (now referred to as pmHS1), from Type A, D, and F *P. multocida* and Type D *P. multocida*, respectively, have been identified and cloned and are disclosed and claimed in co-pending U.S. Serial No. 10/142,143, filed May 8, 2002, and entitled "Heparin/Heparosan Synthase from *P. multocida* and Methods of Making and Using Same", the contents of which are hereby expressly incorporated herein in their entirety. Expression of these single 652-residue and 617-residue, respectively, proteins allows *E. coli* host cells to produce enzymes that polymerize heparosan chains. Laboratory strains of *E. coli* normally do not make heparin. Extracts of recombinant *E. coli*, when supplied with the appropriate UDP-sugars, make heparin *in vitro*. Thus, the pmHS2 and the pmHS1 are authentic heparin synthases.

[00030] It has also been determined that the recombinant pmHAS, pmHS1, pmHS2, and pmCS synthases add sugars to the nonreducing end of a growing polymer chain. The correct monosaccharides are added sequentially in a stepwise fashion to the nascent chain or a suitable exogenous HA or chondroitin oligosaccharide acceptor molecule. The pmHAS sequence, however, is significantly different from the other known HA synthases. There appears to be only two short potential sequence motifs ([D/N]DGS[S/T]; DSD[D/T]Y) in common between pmHAS and the Group A HAS-spHAS. Instead, a portion of the central region of the pmHAS is

more homologous to the amino termini of other bacterial glycosyltransferases that produce different capsular polysaccharides or lipopolysaccharides. Furthermore, pmHAS is about twice as long as any other HAS enzyme.

[00031] When the pmHAS is given long elongation reaction times, HA polymers of at least 400 sugars long are formed. Unlike the Class I HA synthases, recombinant versions of pmHAS and pmCS produced in certain foreign hosts also have the ability to extend exogenously supplied HA or chondroitin oligosaccharides with long HA and chondroitin polymers *in vitro*, respectively. The recombinant pmHS1 and pmHS2 enzymes produced in a foreign host have the ability to extend HA, chondroitin, or heparin oligosaccharides with long heparosan chains *in vitro*. See e.g. U.S. Serial No. 10/195,908, filed July 15, 2002, the contents of which are expressly incorporated herein by reference in their entirety. If recombinant versions of pmHAS or pmCS or pmHS1 or pmHS2 are supplied with functional acceptor oligosaccharides, total HA, chondroitin and heparin biosynthesis is increased up to 50-fold over reactions without the exogenous oligosaccharide. The native versions of the pmHAS, pmCS, pmHS1, and PmHS2 enzymes isolated from *P. multocida* do not perform such elongation reactions with exogenous acceptor (or perform with very low efficiency) due to the presence of a nascent HA, chondroitin, or heparin chain in the natural host. The nature of the polymer retention mechanism of the pmHAS, pmCS, pmHS1, and PmHS2 polypeptide might be the causative factor for this activity: i.e. a HA- or chondroitin- or heparin-binding site may exist that holds onto the HA or chondroitin or heparin chain during polymerization. Small HA or chondroitin or heparin oligosaccharides supplied by the hand of man are also capable of occupying this site of the recombinant enzyme and thereafter be extended into longer polysaccharide chains.

[00032] Most membrane proteins are relatively difficult to study due to their insolubility in aqueous solution, and the native HASs, CSs, HSs, and PmHS2s are no exception. The HAS enzyme from Group A and C *Streptococcus* bacteria has been detergent-solubilized and purified in an active state in small quantities. Once isolated in a relatively pure state, the streptococcal enzyme has very limited stability. A soluble recombinant form of the HAS enzyme from *P. multocida* called $pmHAS^{1-703}$ comprises residues 1-703 of the 972 residues of the native pmHAS enzyme. $pmHAS^{1-703}$ can be mass-produced in *E. coli* and purified by chromatography. The $pmHAS^{1-703}$ enzyme retains the ability of the parent enzyme to add onto either a long HA polymer, a short HA primer, a long chondroitin polymer, a short chondroitin primer, a short chondroitin polymer, as well as other exogenous acceptors. The chondroitin chain may also be sulfated. Furthermore, the purified $pmHAS^{1-703}$ enzyme is stable in an optimized buffer for days on ice and for hours at normal reaction temperatures. One formulation of the optimal buffer consists of 1M ethylene glycol, 0.1 - 0.2 M ammonium sulfate, 50mM Tris, pH 7.2, and protease

inhibitors which also allow the stability and specificity at typical reaction conditions for sugar transfer. For the reaction UDP-sugars and divalent manganese (10-20 mM) are added. $pmHAS^{1-703}$ will also add a HA polymer onto plastic beads with an immobilized short HA primer or any other substrate capable of having an acceptor molecule or acceptor group thereon.

[00033] pmCS, pmHAS, pnHS, and PmHS2 possess two separate glycosyltransferase sites. Protein truncation studies demonstrated that residues 1-117 of pmHAS can be deleted without affecting catalytic activity; similar truncation of the homologous pmCS, pmHS1, and PmHS2 enzymes may also be preferred. The carboxyl-terminal boundary of the GlcUA-transferase of pmHAS resides within residues 686-703 and within residues 686-704 of pmCS. These sites each contain a DGS and DXD motif; all aspartate residues of these motifs are essential for HA synthase activity. D196, D247 and D249 mutants possessed only GlcUA-transferase activity while D477, D527 and D529 mutants possessed only GlcNAc-transferase activity. These results further confirm our previous assignment of the active sites within the synthase polypeptide. The WGGED sequence motif appears to be involved in GlcNAc-transferase activity because E396 mutants and D370 mutants possessed only GlcUA-transferase activity. The highly homologous (90% identical) pmCS can also be mutated in the same fashion. For example, mutating the homologous DXD motif in the GlcUA site of pmCS results in an enzyme with only GalNAc-transferase activity.

[00034] Type F *P. multocida* synthesizes an unsulfated chondroitin (β3N-acetylgalactosamine [GalNAc]-β4GlcUA) capsule. Domain swapping between pmHAS and the homologous chondroitin synthase, pmCS, has been performed. A chimeric or hybrid enzyme consisting of residues 1-427 of pmHAS and residues 421-704 of pmCS was an active HA synthase. On the other hand, the converse chimeric or hybrid enzyme consisting of residues 1-420 of pmCS and residues 428-703 of pmHAS was an active chondroitin synthase. Overall, these findings support the model of two independent transferase sites within a single polypeptide as well as further delineate the site boundaries of both enzymes. The hexosamine-transferase site resides in the N-terminal domain while the GlcUA-transferase site resides in the COOH-terminal domain of these GAG synthases.

[00035] The present invention encompasses methods of producing a variety of unique biocompatible molecules and coatings based on polysaccharides. Polysaccharides, especially those of the glycosaminoglycan class, serve numerous roles in the body as structural elements and signaling molecules. By grafting or making hybrid molecules composed of more than one polymer backbone, it is possible to meld distinct physical and biological properties into a single molecule without resorting to unnatural chemical reactions or residues. The present invention also incorporates the propensity of certain recombinant enzymes, when prepared in a virgin

state, to utilize various acceptor molecules as the seed for further polymer growth: naturally occurring forms of the enzyme or existing living wild-type host organisms do not display this ability. Thus, the present invention results in (a) the production of hybrid oligosaccharides or polysaccharides and (b) the formation of polysaccharide coatings. Such hybrid polymers can serve as "molecular glue" -- i.e. when two cell types or other biomaterials interact with each half of a hybrid molecule, then each of the two phases are bridged.

[00036] Such polysaccharide coatings are useful for integrating a foreign object within a surrounding tissue matrix. For example, a prosthetic device is more firmly attached to the body when the device is coated with a naturally adhesive polysaccharide. Additionally, the device's artificial components could be masked by the biocompatible coating to reduce immunoreactivity or inflammation. Another aspect of the present invention is the coating or grafting of GAGs onto various drug delivery matrices or bioadhesives or suitable medicaments to improve and/or alter delivery, half-life, persistence, targeting and/or toxicity.

[00037] Recombinant pmHAS, pmCS, pmHS1, and PmHS2 elongate exogenous functional oligosaccharide acceptors to form long or short polymers *in vitro*; thus far no other Class I HA synthase has displayed this capability. The directionality of synthesis was established definitively by testing the ability of pmHAS and pmCS and pmHS1 and PmHS2 to elongate defined oligosaccharide derivatives. The non-reducing end sugar addition allows the reducing end to be modified for other purposes; the addition of GAG chains to small molecules, polymers, or surfaces is thus readily performed. Analysis of the initial stages of synthesis demonstrated that pmHAS and pmCS and pmHS1 and PmHS2 added single monosaccharide units sequentially. Apparently the fidelity of the individual sugar transfer reactions is sufficient to generate the authentic repeating structure of HA or chondroitin or heparin. Therefore, simultaneous addition of disaccharide block units is not required as hypothesized in some recent models of polysaccharide biosynthesis. pmHAS and pmCS and pmHS1 and PmHS2 appear distinct from most other known HA and chondroitin and heparin synthases based on differences in sequence, topology in the membrane, and/or putative reaction mechanism.

[00038] As mentioned previously, pmHAS, the 972-residue membrane-associated hyaluronan synthase, catalyzes the transfer of both GlcNAc and GlcUA to form an HA polymer. In order to define the catalytic and membrane-associated domains, pmHAS and pmCS mutants have been analyzed. $pmHAS^{1-703}$ is a soluble, active HA synthase suggesting that the carboxyl-terminus is involved in membrane association of the native enzyme. $pmHAS^{1-650}$ is inactive as a HA synthase, but retains GlcNAc-transferase activity. Within the pmHAS sequence, there is a duplicated domain containing a short motif, DGS or Asp-Gly-Ser, that is conserved among many glycosyltransferases. Changing this aspartate in either domain to asparagine, glutamate, or

lysine reduced the HA synthase activity to low levels. The mutants substituted at residue 196 possessed GlcUA-transferase activity while those substituted at residue 477 possessed GlcNAc-transferase activity. The Michaelis constants of the functional transferase activity of the various mutants, a measure of the apparent affinity of the enzymes for the precursors, were similar to wild-type values. Furthermore, mixing D196N and D477K mutant proteins in the same reaction allowed HA polymerization at levels similar to the wild-type enzyme. These results provide the first direct evidence that the synthase polypeptide utilizes two separate glycosyltransferase sites. Likewise, pmCS mutants were made and tested having the same functionality and sequence similarity to the mutants created for pmHAS.

[00039] *Pasteurella multocida* Type F, the minor fowl cholera pathogen, produces an extracellular polysaccharide capsule that is a putative virulence factor. As outlined in U.S. Serial No. 09/842,484, filed April 25, 2002, and entitled "Chondroitin Synthase Gene and Methods of Making and Using Same", the contents of which are hereby expressly incorporated herein in their entirety, the capsule of *Pasteurella multocida* Type F was removed by treating microbes with chondroitin AC lyase. It was found by acid hydrolysis that the polysaccharide contained galactosamine and glucuronic acid. A Type F polysaccharide synthase was molecularly cloned and its enzymatic activity was characterized. The 965-residue enzyme, called pmCS, is 90% identical at the nucleotide and the amino acid level to the hyaluronan synthase, pmHAS, from *P. multocida* Type A. A recombinant *Escherichia coli*-derived, truncated, soluble version of pmCS (residues 1-704) was shown to catalyze the repetitive addition of sugars from UDP-GalNAc and UDP-GlcUA to chondroitin oligosaccharide acceptors *in vitro*. Other structurally related sugar nucleotide precursors did not substitute in the elongation reaction. Polymer molecules composed of $\sim 10^3$ sugar residues were produced as measured by gel filtration chromatography. The polysaccharide synthesized *in vitro* was sensitive to the action of chondroitin AC lyase but resistant to the action of hyaluronan lyase. This was the first report identifying a glycosyltransferase that forms a polysaccharide composed of chondroitin disaccharide repeats, $[\beta(1,4)\text{GlcUA-}\beta(1,3)\text{GalNAc}]_n$. In analogy to known hyaluronan synthases, a single polypeptide species, pmCS, possesses both transferase activities. The heparin synthases, pmHS1 and PmHS2, from *P. multocida*, also are a single polypeptide specie that possess both transferase activities to catalyze heparin/heparosan.

[00040] Promising initial target polymers for a variety of therpaeutic uses are glycosaminoglycan chains composed of about 5 kDa to about 4 MDa. The two current competing state-of-the-art techniques for creating the desired smaller size glycosaminoglycan [GAG] polymers are extremely limited and will not allow the medical potential of the sugars to be achieved. Small GAG molecules are presently made either by: (1) partially depolymerizing

costly large polymers with degradative enzymes or with chemical means (e.g. heat, acid, sonication), or (2) highly demanding organic chemistry-based carbohydrate synthesis. The former method is difficult to control, inefficient, costly, and is in a relatively stagnant development stage. For example, the enzyme wants to degrade the polymer to the 2 or 4 sugar end stage product, but this sugar is inactive for many therapeutic treatments. The use of acid hydrolysis also removes a fraction of the acetyl groups from the GlcNAc or GalNAc groups thereby introducing a positive charge into an otherwise anionic molecule. The latter method, chemical synthesis, involves steps with low to moderate repetitive yield and has never been reported for a HA-oligosaccharide longer than 6 to 8 sugars in length. Also racemization (e.g. production of the wrong isomer) during chemical synthesis creates inactive or harmful molecules; the inclusion of the wrong isomer in a therapeutic preparation in the past has had tragic consequences as evidenced by the birth defects spawned by the drug Thalidomide. As sugars contain many similar reactive hydroxyl groups, in order to effect proper coupling between two sugars in a chemical synthesis, most hydroxyl groups must be blocked or protected. At the conclusion of the reaction, all of the protecting groups must be removed, but this process is not perfect; as a result, a fraction of the product molecules retain these unnatural moieties. The issues of racemization and side-products from chemical synthesis are not problems for the high-fidelity enzyme catalysts of the presently claimed and disclosed invention.

[00041] The partial depolymerization method only yields fragments of the original GAG polymer and is essentially useless for creating novel sugars beyond simple derivatizations (e.g. esterifying some fraction of GlcUA residues in an indiscriminate fashion). Chemical synthesis may suffice in theory to make novel sugars, but the strategy needs to be customized for adding a new sugar, plus the problems with side-reactions/isomerization and the ultimate oligosaccharide size still pose the same trouble as described earlier. Another distinct method using the degradative enzymes to generate small molecules by "running in reverse" on mixtures of two polymers (e.g. HA and chondroitin) has some potential for novel GAG polysaccharide synthesis. See e.g. J Biochem (Tokyo). 2000 Apr;127(4):695-702, Chimeric glycosaminoglycan oligosaccharides synthesized by enzymatic reconstruction and their use in substrate specificity determination of Streptococcus hyaluronidase, Takagaki K, Munakata H, Majima M, Kakizaki I, Endo M.; and J Biol Chem. 1995 Feb 24;270(8):3741-7, Enzymic reconstruction of glycosaminoglycan oligosaccharide chains using the transglycosylation reaction of bovine testicular hyaluronidase, Saitoh H, Takagaki K, Majima M, Nakamura T, Matsuki A, Kasai M, Narita H, Endo M. However, this technology can make only a very limited scope of products with a block pattern (no single or specifically spaced substitutions possible) using slow reactions that

cannot easily be customized or controlled. No other technology is as versatile as the presently claimed and disclosed biocatalytic system with respect to flexibility of final polysaccharide structure in the about 5 kDa to about 4 MDa size range. Novel, "designer" molecules can be prepared with minimal re-tooling by use of the appropriate hyaluronic acid or chondroitin or heparin enzyme catalysts and substrates.

[00042] The size of the HA polysaccharide dictates its biological effect in many cellular and tissue systems based on many reports in the literature. However, no source of very defined, uniform HA polymers with sizes greater than 5 kDa is currently available. This situation is complicated by the observation that long and short HA polymers appear to have antagonistic or inverse effects on some biological systems. Therefore, HA preparations containing a mixture of both size populations may yield contradictory or paradoxical results. Thus, one of the objects of the present invention is to provide a method to produce HA with very narrow, substantially monodisperse size distributions that overcomes the disadvantages and defects of the prior art.

[00043] The methods for enzymatically producing defined glycosaminoglycan polymers of the present invention involves providing at least one functional acceptor and at least one recombinant glycosaminoglycan transferase capable of elongating the functional acceptor in a controlled or repetitive fashion to form extended glycosaminoglycan-like molecules. At least one of UDP-GlcUA, UDP-GalUA UDP-GlcNAc, UDP-Glc, UDP-GalNAc, UDP-GlcN, UDP-GalN and a structural variant or derivative thereof is added in a stoichiometric ratio to the functional acceptor to provide glycosaminoglycan polymers that are substantially monodisperse in size.

[00044] The term "substantially monodisperse in size" as used herein will be understood to refer to defined glycoasminoglycan polymers that have a very narrow size distribution. For example, substantially monodisperse glycosaminoglycan polymers having a molecular weight in a range of from about 3.5 kDa to about 0.5 MDa will have a polydispersity value (i.e. Mw/Mn, where Mw is the average molecular weight and Mn is the number average molecular weight) in a range of from about 1.0 to about 1.1, and preferably in a range from about 1.0 to about 1.05. In yet another example, substantially monodisperse glycosaminoglycan polymers having a molecular weight in a range of from about 0.5 MDa to about 4.5 MDa will have a polydispersity value in a range of from about 1.0 to about 1.5, and preferably in a range from about 1.0 to about 1.2.

[00045] The functional acceptor utilized in accordance with the present invention will have at least two sugar units of uronic acid and/or hexosamine, wherein the uronic acid may be GlcUA, IdoUA or GalUA, and the hexosamine may be GlcNAc, GalNAc, GlcN or GalN. In one embodiment, the functional acceptor may be an HA oligosaccharide of about 3 sugar units to

about 4.2 kDa, or an HA polymer having a mass of about 3.5 kDa to about 2MDa. In another embodiment, the functional acceptor may be a chondroitin oligosaccharide or polymer, a chondroitin sulfate oligosaccharide or polymer, or a heparosan-like polymer. In yet another embodiment, the functional acceptor may be an extended acceptor such as HA chains, chondroitin chains, heparosan chains, mixed glycosaminoglycan chains, analog containing chains or any combination thereof.

[00046] Any recombinant glycosaminoglycan transferase described or incorporated by reference herein may be utilized in the methods of the present invention. For example, the recombinant glycosaminoglycan transferase utilized in accordance with the present invention may be a recombinant hyaluronan synthase, a recombinant chondroitin synthase, a recombinant heparosan synthase, or any active fragment or mutant thereof. The recombinant glycosaminglycan transferase may be capable of adding only one UDP-sugar described herein above or may be capable of adding two or more UDP-sugars described herein above.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

[00047] FIG. 1 is a graphical representation showing that an HA tetramer stimulates pmHAS polymerization.

[00048] FIG. 2 is a graphical plot showing that HA polymerization is effected by HA oligosaccharides.

[00049] FIG. 3 is a graphical plot showing HA tetramer elongation into larger polymers by pmHAS.

[00050] FIG. 4 is a graphical representation of a thin layer chromatography analysis of pmHAS extension of HA tetramer.

[00051] FIG. 5 is a graphical representation of thin layer chromatography analysis of the early stages of HA elongation.

[00052] FIG. 6 is an electrophoresis gel showing the purification of $pmHAS^{1-703}$.

[00053] FIG. 7 is a pictorial representation of the pmHAS truncation mutants.

[00054] FIG. 8 is a Southern Blot showing the hybridization of the pmCS gene with the *KfoC* gene.

[00055] FIG. 9 is a Western Blot analysis showing the expression of pmHAS and its truncated forms. Either whole cell lysates ($pmHAS^{437-972}$, $pmHAS^{1-567}$, and $pmHAS^{152-756}$) or membrane preparations ($pmHAS^{437-756}$, $pmHAS^{1-567}$, **r**1-972, **n**1-972) or B-Per extract ($pmHAS^{1-703}$) were analyzed by Western blot (**r**,recombinant from *E. coli*; **n**, native from P-1059). The *bars* on the left denote the position of molecular weight standards (from top to bottom: 112, 95, 55, and 29 kDa).

[00056] FIG. 10 is a pictorial representation of domains A1 and A2 of pmHAS. **(A)** The approximate relative positions of domain A1 and A2 in pmHAS and pmHAS$^{1-703}$. **(B)** Partial alignment of the amino acid sequences of the two domains (residue 161-267 and 443-547). The aspartate residues mutated in our studies were marked with *. Identical residues are in **bold.**

[00057] FIG. 11 is a graphical representation of the complementation of the HAS activity of mutant enzymes *in vitro*. HAS enzyme assays with HA-derived acceptor were performed in the presence of either wild type pmHAS$^{1-703}$ alone, or D196 mutant alone, or D477 mutant alone or in the presence of both D196 and D477 mutants, for either 25 minutes (*open bars*) or 1.5 hours (*solid bars*).

[00058] FIG. 12 is a sequence alignment of pmCS and pmHAS. The two *Pasteurella* GAG synthases are highly homologous. Identical residues are denoted with the *hyphen*. The numbering scheme corresponds to the slightly longer pmHAS sequence. The putative A1 (residues 161-267) and A2 (residues 443-547) domains correspond to regions important for hexosamine transferase or for glucuronic acid transferase activity, respectively (33). Most sequence differences are found in the amino-terminal half of the polypeptides.

[00059] FIG. 13 is a pictorial representation of a model of the two putative glycosyltransferase sites of pmHAS and pmCS. PmHAS and pmCS contain two distinct and relatively independent glycosyltransferase sites. Each site possesses a DGS and a DXD amino acid motif. A WGGED motif is found near the junction of the two domains, and is involved in hexosamine-transferase activity. The carboxyl-terminus is involved in membrane association (MEM ASSOC), but is not required for catalytic activity. Residues 1-117 (*cross-hatched*) appear dispensable for catalysis of sugar transfer but may contain structure scaffolding or play other roles.

[00060] FIG. 14 graphically depicts Sequence Similarity of pmHS1 with KfiA and KfiC. Elements of the *Pasteurella* heparosan synthase, HS1 (containing residues 91-240) and HS2 (containing residues 441-540) are very similar to portions of two proteins from the *E. coli* K5 capsular locus (A, residues 75-172 of KfiA; C, residues 262- 410 of KfiC) as shown by this modified Multalin alignment (ref. 21; numbering scheme corresponds to the pmHS1 sequence). The HS1 and HS2 elements may be important for hexosamine transferase or for glucuronic acid transferase activities, respectively. (con, consensus symbols: asterisks, [K or R] and [S or T]; %, any one of F,Y,W; $, any one of L,M; !, any one of I,V; #, any one of E,D,Q,N).

[00061] FIG. 15(A-D) graphically depicts the alignment of the pmHS1 (two clones: A2, B10) with PmHS2, KfiA, KfiC, and DcbF. pmHS1 is shown in various forms: HSA1 and HSA2 are the two putative domains of pmHS1; pORF = partial open reading frame which was obtained before

complete sequence determined; recon = reconstructed open reading frame with sequence from multiple sources.

[00062] FIG. 16 depicts chimeric constructs of pm-EG, pm-FH, pm-IK, and pm-JL. PCR-overlap-extension was performed. Pm-EG contains residues 1-265 from pmHAS and residues 259-704 from pmCS and is a GlcUA-Tase. Pm-FH contains residues 1-258 from pmCS and residues 266-703 from pmHAS and is an active chondrotin synthase. Pm-IK contains residues 1-221 from pmHAS and residues 215-704 from pmCS and is a Glc-UA-Tase. Pm-JL contains residues 1-214 from pmCS and residues 222-703 from pmHAS and is an active HA synthase. The switch of Gal-NAc-transferring activity into GlcNAc-transferring activity indicated that 222-265 of pmHAS and possibly the corresponding residues 215-258 of pmCS play critical role in the selectivity between binding and/or transferring of GalNAc and GlcNAc substrate.

[00063] FIG. 17 depicts a comparison of partial primary sequences of pmHAS and different pmCSs. Primary sequences of presumably chondroitin synthases from different Type F *Pasteruella multocida* were obtained by directly sequencing the products of colony-lysis PCR. The MULTALIN alignment indicates that most of the differences between pmHAS and pmCS are conserved among these independent strains. Residues that were substituted in site-mutagenesis studies were underlined. The mutant polypeptides contain a single or combination of different mutations, indicated by *star(s)*. None of these mutations changes the specificity of the original enzymes.

[00064] FIG. 18 depicts chimeric constructs of $pmHAS^{1-221}$-$CS^{215-258}$-$HAS^{266-703}$ and $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$. Pm-FH and pPm7A DNA were used to create $pmHAS^{1-221}$-$CS^{215-258}$-$HAS^{266-703}$. A very interesting result was that $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$ can transfer both GalNAc and GlcNAc to HA oligomer acceptor; this enzyme displays relaxed sugar specificity.

[00065] FIG. 19 depicts a summary of enzyme activities of chimeric proteins. The enzymes are drawn as bars. *Black* bars represent pmCS. *White* bars represent pmHAS. +, active; -, inactive. PmCHC represents $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$. The roles of the two domains are confirmed and we have localized a 44-residue region critical for distinguishing C4 epimers of the hexosamine precursor.

[00066] FIG. 20 is a graphical representation illustrating *in vitro* HA synthesis in the presence or absence of HA4 acceptor. Reactions were carried out at 30°C for 48 hours. The 100 µl reaction contains 1µg/µl of pmHAS, 30mM UDP-GlcNAc, 30mM UDP-GlcUA and with (lane 3) or without (lane 4) 0.03µg/µl of HA4. 0.2 µl of reactions were loaded on 0.7% agarose gel and stained with STAINS-ALL. Lane 1, 3 µg of HA from Genzyme. Lane 2, DNA of BIOLINE HyperLadder (from top to bottom is 10 kb, 8kb, 6kb, 5kb, 4kb, 3kb, 2.5kb, 2kb, 1.5kb, 1kb, 800bp, 600bp, 400bp, 200bp). Lane 5, Invitrogen high-Mw DNA ladder (top band is 48.5 kb).

[00067] FIG. 21 are electrophoresis gels illustrating intermediate size HA polysaccharides as acceptors. The starting 20 µl reaction contain15 µg of pmHAS, 10 mM UDP-sugars and 5 µg HA4. 5µl of 40 mM UDP-sugars and 15µg of pmHAS were supplied additionally every 48 hours ("feeding'). A. 0.1% agarose gel electrophoresis. Lane 1, 3 feedings. Lane 2, 2 feedings. Lane3, one feedings. Lane 4, no feeding. D1, Bio-Rad 1kb DNA ruler. D2 Lambda HindIII DNA. D3, Bio-Rad 100bp DNA ruler. B. 15% acrylamide gel electrophoresis. Lane1-4, same as in panel A.

[00068] FIG. 22 is a graphical representation of a model of *Pasteurella* synthase polymerization.

[00069] FIG. 23 is a graphical representation of a model of reaction synchronization.

[00070] FIG. 24 is a graphical representation of a model of stoichiometric control of polymer size.

[00071] FIG. 25 is an electrophoresis gel illustrating that *in vitro* generated HA can reach the molecular mass of 1.3 MDa. The reaction condition is the same as in FIG. 31 except with 0.2 µg of HA4. 1.2 µg of purified HA was loaded on 1.0 % agarose gel. Lane 2, Bio-Rad 1 kilobase DNA ruler with the top band of 15 kb. Lane 3, Bioline DNA hyperLadder with the top band of 10 kb.

[00072] FIG. 26 is a graphical representation illustrating control of HA product size by acceptor concentration. 100 µl of reactions were setup with 0.7 µg/µl of pmHAS, 32mM of UDP-GlcNAc, 32mM of UDP-GlcUA and decreasing amount of HA4. HA were purified as described and 1µg of each sample were loaded on a 1.2% agarose gel (A). The molecular mass of HA were determined by MALLS and the results were listed in the table (B). The item numbers in the table correspond to lane number in Panel A. M, Bioline DNA HyperLadder.

[00073] FIG. 27 is an electrophoresis gel illustrating *in vitro* synthesis of fluorescent HA. 20 µl of reactions were setup with 2 µg/µl of pmHAS, various amounts of fluorescent HA4 and UDP-sugars. Reaction products were analyzed with 0.8% agarose gel electrophoresis and viewed under UV light.

[00074] FIG. 28 is an electrophoresis gel illustrating utilization of large HA acceptors. Reactions were carried out at 30°C for 48 hours. The 60 µl reaction contained 0.28 µg/µl of pmHAS, 3.3 mM UDP-GlcNAc, 3.3 mM UDP-GlcUA and without (lane 2) or with various amounts of acceptors (lanes 3-5, 7-9 and 10). 1.0 µl of each reaction was loaded on 0.7% agarose gel and stained with STAINS-ALL. Lane 1, BIORAD kb ladder (top band is 15 kb). Lane 6, 0.5 µg of 970 kDa HA starting acceptor. Lane 11, 3 µg of Genzyme HA starting acceptor. Lane 12, Invitrogen DNA HyperLadder (top band is 48.5 kB).

[00075] FIG. 29 is an electrophoresis gel that illustrates the migration of a ladder constructed of HA of defined size distribution for use as a standard.

[00076] FIG. 30 is an electrophoresis gel illustrating various mondisperse chondroitin sulfate HA hybrid GAGs. The 1% agarose gel stained with STAINS-ALL shows a variety of chondroitin sulfates (either A, B or C) that were elongated with pmHAS, thus adding HA chains. Lanes 1, 8, 15, 22 and 27 contain the Kilobase DNA ladder; lanes 2 and 7 contain starting CSA, while lanes 3-6 contain CSA-HA at 2 hrs, 4 hrs, 6 hrs and O/N, respectively; lanes 9 and 14 contain starting CSB, while lanes 10-13 contain CSB-HA at 2 hrs, 4 hrs, 6 hrs and O/N, respectively; lanes 16 and 21 contain starting CSC, while lanes 17-20 contain CSC-HA at 2 hrs, 4 hrs, 6 hrs and O/N, respectively; lanes 23-26 contain no acceptor at 2 hrs, 4 hrs, 6 hrs and O/N, respectively.

[00077] FIG. 31 is an electrophoresis gel illustrating control of hybrid GAG size by stoichiometric control. The 1% agarose gel stained with STAINS-ALL shows chondroitin sulfate A that was elongated with pmHAS, thus adding HA chains. Lanes 1, 7, 13, 19 and 25 contain the Kilobase ladder; lanes 2 and 6 contain 225 µg starting CSA, while lanes 3-5 contain 225 µg CSA-HA at 2 hrs, 6 hrs and O/N, respectively; lanes 8 and 12 contain 75 µg starting CSA, while lanes 9-11 contain 75 µg CSA-HA at 2 hrs, 6 hrs and O/N, respectively; lanes 14 and 18 contain 25 µg starting CSA, while lanes 15-17 contain 25 µg CSA-HA at 2 hrs, 6 hrs and O/N, respectively; lanes 20 and 24 contain 8.3 µg starting CSA, while lanes 21-23 contain 8.3 µg CSA-HA at 2 hrs, 6 hrs and O/N, respectively.

[00078] FIG. 32 is an electrophoresis gel illustrating extension of HA with chondroitin chains using pmCS. The 1.2% agarose gel stained with STAINS-ALL shows a reaction with pmCS and UDP-GlcUA, UDP-GalNAC with eithera 81 kDa HA acceptor (lanes 3-7) or no acceptor (lanes 9-13). Lanes 1 and 15 contain the Kilobase DNA standard. Lanes 2, 8 and 14 contain starting 81 kDa HA. Lanes 3-7: contain HA acceptor +HA-C at 2 hr, 4 hr, 4 hr (set O/N in incubator without 4 hr feeding), 6 hr and O/N, respectively. Lanes 9-13: contain no acceptor (minus) -HA-C at 2 hr, 4 hr, 4 hr (set O/N in incubator without 4 hr feeding), 6 hr and O/N, respectively.

[00079] FIG. 33. Size exclusion (or gel filtration) chromatography analysis coupled with multi-angle laser light scattering detection confirms the monodisperse nature of polymers created by the present invention. In A, HA (starting MW 81 kDa) extended with chondroitin chains using pmCS (same sample used in Fig 32 lane #7, overnight [O/N] extension) was analyzed; the material was 280,000 Mw and polydispersity (Mw/Mn) was 1.003 +/- 0.024. Chondroitin sulfate extended with HA chains using pmHAS (same sample used in Fig 31, lane

#23) was analyzed and shown in the bottom chromatogram; the material was 427,000 Mw and polydispersity (Mw/Mn) was 1.006 +/- 0.024.

[00080] FIG. 34 is an 0.7% agarose gel detected with Stains-all compares the monodisperse, 'select HA' to commercially produced HA samples.

DETAILED DESCRIPTION OF THE INVENTION

[00081] Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not limited in its application to the details of construction and the arrangements of the components set forth in the following description or illustrated in the drawings. The invention is capable of other embodiments or of being practiced or carried out in various ways. Also, it is to be understood that the phraseology and terminology employed herein is for purpose of description and should not be regarded as limiting.

[00082] Glycosaminoglycans ("GAGs") are linear polysaccharides composed of repeating disaccharide units containing a derivative of an amino sugar (either glucosamine or galactosamine). Hyaluronan [HA], chondroitin, and heparan sulfate/heparin contain a uronic acid as the other component of the disaccharide repeat while keratan contains a galactose. The GAGs are summarized in Table I.

Table I

Polymer	Disaccharide Repeat	Post-Polymerization Modifications	
		Vertebrates	Bacteria
Hyaluronan	β3GlcNAc β4GlcUA	none	none
Chondroitin	β3GalNAc β4GlcUA	O-sulfated/epimerized	none
Heparin/heparan	α4GlcNAc β4GlcUA	O,N-sulfated/epimerized	none
Keratan	β4GlcNAc β3Gal	O-sulfated	not reported

[00083] Vertebrates may contain all four types of GAGs, but the polysaccharide chain is often further modified after sugar polymerization. One or more modifications including O-sulfation of certain hydroxyls, deacetylation and subsequent N-sulfation, or epimerization of glucuronic acid to iduronic acid are found in most GAGs except HA. An amazing variety of distinct structures have been reported for chondroitin sulfate and heparan sulfate/heparin even within a single polymer chain. A few clever pathogenic microbes also produce unmodified GAG chains; the bacteria use extracellular polysaccharide coatings as molecular camouflage to avoid host defenses. The chondroitin and heparan sulfate/heparin chains in vertebrates are initially synthesized by elongation of a xylose-containing linkage tetrasaccharide attached to a variety of proteins. Keratan is either O-linked or N-linked to certain proteins depending on the particular molecule. HA and all of the known bacterial GAGs are not part of the classification of proteins known as glycoproteins. All GAGs except HA are found covalently linked to a core

protein, and such combination is referred to as a proteoglycan. Glycoproteins are usually much smaller than proteoglycans and only contain from 1-60% carbohydrate by weight in the form of numerous relatively short, branched oligosaccharide chains, whereas a proteoglycan can contain as much as 95% carbohydrate by weight. The core protein in a proteoglycan is also usually a glycoprotein, therefore usually contains other oligosaccharide chains besides the GAGs.

[00084] GAGs and their derivatives are currently used in the medical field as ophthalmic and viscoelastic supplements, adhesion surgical aids to prevent post-operative adhesions, catheter and device coatings, and anticoagulants. Other current or promising future applications include anti-cancer medications, tissue engineering matrices, immune and neural cell modulators, and drug targeting agents.

[00085] Complex carbohydrates, such as GAGs, are information rich molecules. A major purpose of the sugars that make up GAGs is to allow communication between cells and extracellular components of multicellular organisms. Typically, certain proteins bind to particular sugar chains in a very selective fashion. A protein may simply adhere to the sugar, but quite often the protein's intrinsic activity may be altered and/or the protein transmits a signal to the cell to modulate its behavior. For example, in the blood coagulation cascade, heparin binding to inhibitory proteins helps shuts down the clotting response. In another case, HA binds to cells via the CD44 receptor that stimulates the cells to migrate and to proliferate. Even though long GAG polymers (i.e. $>10^2$ Da) are found naturally in the body, typically the protein's binding site interacts with a stretch of 4 to 10 monosaccharides. Therefore, oligosaccharides can be used to either (a) substitute for the polymer or (b) to inhibit the polymer's action depending on the particular system.

[00086] HA polysaccharide plays structural roles in the eye, skin, and joint synovium. Large HA polymers ($\sim 10^6$ Da) also stimulate cell motility and proliferation. On the other hand, shorter HA polymers ($\sim 10^4$ Da) often have the opposite effect. HA-oligosaccharides composed of 10 to 14 sugars [HA_{10-14}] have promise for inhibition of cancer cell growth and metastasis. In an *in vivo* assay, mice injected with various invasive and virulent tumor cell lines (melanoma, glioma, carcinomas from lung, breast and ovary) develop a number of large tumors and die within weeks. Treatment with HA oligosaccharides greatly reduced the number and the size of tumors. Metastasis, the escape of cancer cells throughout the body, is one of the biggest fears of both the ailing patient and the physician. HA or HA-like oligosaccharides appear to serve as a supplemental treatment to inhibit cancer growth and metatasis.

[00087] The preliminary mode of action of the HA-oligosaccharide sugars is thought to be mediated by binding or interacting with one of several important HA-binding proteins (probably

CD44 or RHAM) in the mammalian body. One proposed scenario for the anticancer action of HA-oligosaccharides is that multiple CD44 protein molecules in a cancer cell can bind simultaneously to a long HA polymer. This multivalent HA binding causes CD44 activation (perhaps mediated by dimerization or a receptor patching event) that triggers cancer cell activation and migration. However, if the cancer cell is flooded with small HA-oligosaccharides, then each CD44 molecule individually binds a different HA molecule in a monovalent manner such that no dimerization/patching event occurs. Thus no activation signal is transmitted to the cell. Currently, it is believed that the optimal HA-sugar size is 10 to 14 sugars. Although this size may be based more upon the size of HA currently available for testing rather than biological functionality - i.e. now that HA molecules and HA-like derivatives <10 sugars are available according to the methodologies of the present invention, the optimal HA size or oligosaccharide composition may be found to be different.

[00088] It has also been shown that treatment with certain anti-CD44 antibodies or CD44-antisense nucleic acid prevents the growth and metastasis of cancer cells in a fashion similar to HA-oligosaccharides; in comparison to the sugars, however, these protein-based and nucleic acid-based reagents are somewhat difficult to deliver in the body and/or may have long-term negative effects. A very desirable attribute of HA-oligosaccharides for therapeutics is that these sugar molecules are natural by-products that can occur in small amounts in the healthy human body during the degradation of HA polymer; no untoward innate toxicity, antigenicity, or allergenic concerns are obvious.

[00089] Other emerging areas for the potential therapeutic use of HA oligosaccharides are the stimulation of blood vessel formation and the stimulation of dendritic cell maturation. Enhancement of wound-healing and resupplying cardiac oxygenation may be additional applications that harness the ability of HA oligosaccharides to cause endothelial cells to form tubes and sprout new vessels. Dendritic cells possess adjuvant activity in stimulating specific CD4 and CD8 T cell responses. Therefore, dendritic cells are targets in vaccine development strategies for the prevention and treatment of infections, allograft reactions, allergic and autoimmune diseases, and cancer.

[00090] Heparin interacts with many proteins in the body, but two extremely interesting classes are coagulation cascade proteins and growth factors. Antithrombin III [ATIII] and certain other hemostasis proteins are 100,000-fold more potent inhibitors of blood clotting when complexed with heparin. Indeed, heparin is so potent it must be used in a hospital setting and require careful monitoring in order to avoid hemorrhage. Newer, processed lower molecular weight forms of heparin are safer, but this material is still a complex mixture. It has been shown that a particular pentasaccharide (5 sugars long) found in heparin is responsible

for the ATIII-anticoagulant effect. But since heparin is a very heterogeneous polymer, it is difficult to isolate the pentasaccharide (5 sugars long) in a pure state. The pentasaccharide can also be prepared in a conventional chemical synthesis involving ~50 to 60 steps. However, altering the synthesis or preparing an assortment of analogs in parallel is not always feasible - either chemically or financially.

[00091] Many growth factors, including VEGF (vascular endothelial growth factor), HBEGF (heparin-binding epidermal growth factor), and FGF (fibroblast growth factor), bind to cells by interacting simultaneously with the growth factor receptor and a cell-surface heparin proteoglycan; without the heparin moiety, the potency of the growth factor plummets. Cell proliferation is modulated in part by heparin; therefore, diseases such as cancer and atherosclerosis are potential targets. Abnormal or unwanted proliferation would be curtailed if the growth factor was prevented from stimulating target disease-state cells by interacting with a heparin-like oligosaccharide analog instead of a surface-bound receptor. Alternatively, in certain cases, the heparin oligosaccharides alone have been shown to have stimulatory effects.

[00092] Chondroitin is the most abundant GAG in the human body, but all of its specific biological roles are not yet clear. Phenomenon such as neural cell outgrowth appear to be modulated by chondroitin. Both stimulatory and inhibitory effects have been noted depending on the chondroitin form and the cell type. Therefore, chondroitin or similar molecules are of utility in re-wiring synaptic connections after degenerative diseases (e.g. Alzheimer's) or paralytic trauma. The epimerized form of chondroitin (GlcUA converted to the C5 isomer, iduronic acid or IdoUA), dermatan, selectively inhibits certain coagulation proteins such as heparin cofactor II. By modulating this protein in the coagulation pathway instead of ATIII, dermatan appears to allow for a larger safety margin than heparin treatment for reduction of thrombi or clots that provoke strokes and heart attacks.

[00093] Many details of GAG/protein interactions are not yet clear due to (a) the heterogeneity of GAGs (in part due to their biosynthesis pathway) and (b) the difficulty in analyzing long polysaccharides and membrane receptor proteins at the molecular level. Fortunately, many short oligosaccharides have biological activities that serve to assist research pursuits as well as to treat disease in the near future. Conventional chemical synthesis of short GAG oligosaccharides is possible, but the list of roadblocks includes: (i) difficult multi-step syntheses that employ toxic catalysts, (ii) very low yield or high failure rates with products longer than ~6 monosaccharides, (iii) imperfect control of stereoselectivity (e.g. wrong anomer) and regioselectivity (e.g. wrong attachment site), and (iv) the possibility for residual protection groups (non-carbohydrate moieties) in the final product.

[00094] Chemoenzymatic synthesis, however, employing catalytic glycosyltransferases with exquisite control and superb efficiency is currently being developed by several universities and companies. A major obstacle is the production of useful catalyst because the vast majority of glycosyltransferases are rare membrane proteins that are not particularly robust. In the copending applications referenced herein and in the presently claimed and disclosed invention, several practical catalysts from *Pasteurella* bacteria that allow for the synthesis of the three most important human GAGs (i.e. the three known acidic GAGs) are described and enabled (e.g. HA, chondroitin, and heparin).

[00095] All of the known HA, chondroitin and heparan sulfate/heparin glycosyltransferase enzymes that synthesize the alternating sugar repeat backbones in microbes and in vertebrates utilize UDP-sugar precursors and divalent metal cofactors (e.g. magnesium, cobalt, and/or manganese ion) near neutral pH according to the overall reaction:

$$n\text{UDP-GlcUA} + n\text{UDP-HexNAc} \rightarrow 2n\text{UDP} + [\text{GlcUA-HexNAc}]_n$$

where HexNAc = GlcNAc or GalNAc. Depending on the specific GAG and the particular organism or tissue examined, the degree of polymerization, n, ranges from about 25 to about 10,000. If the GAG is polymerized by a single polypeptide, the enzyme is called a synthase or co-polymerase.

[00096] As outlined in copending and incorporated by reference in the "Cross-Reference" section of this application hereinabove, the present applicant(s) have discovered four new dual-action enzyme catalysts from distinct isolates of the Gram-negative bacterium *Pasteurella multocida* using various molecular biology strategies. *P. multocida* infects fowl, swine, and cattle as well as many wildlife species. The enzymes are: a HA synthase, or (pmHAS); a chondroitin synthase, or (pmCS); and two heparosan synthases, or (pmHS1 and PmHS2). To date, no keratan synthase from any source has been identified or reported in the literature.

[00097] In copending U.S. Serial No. 10/217,613, filed August 12, 2002, the contents of which are hereby expressly incorporated herein by reference in their entirety, the molecular directionality of pmHAS synthesis was disclosed and claimed. pmHAS is unique in comparison to all other existing HA synthases of *Streptococcus* bacteria, humans and an algal virus. Specifically, recombinant pmHAS can elongate exogeneously-supplied short HA chains (e.g. 2-4 sugars) into longer HA chains (e.g. 3 to 150 sugars). The pmHAS synthase has been shown to add monosaccharides one at a time in a step-wise fashion to the growing chain. The pmHAS enzyme's exquisite sugar transfer specificity results in the repeating sugar backbone of the GAG chain. The pmCS enzyme, which is about 90% identical at the amino acid level to pmHAS, performs the same synthesis reactions but transfers GalNAc instead of GlcNAc. The pmCS enzyme was described and enabled in copending U.S. Serial No. 09/842,484. The pmHS1 and

PmHS2 enzymes are not very similar at the amino acid level to pmHAS, but perform the similar synthesis reactions; the composition of sugars is identical but the linkages differ because heparosan is Beta4GlcUA-alpha4GlcNAc. The pmHS1 and PmHS2 enzymes were described and enabled in copending U.S. Serial No. 10/142,143.

[00098] The explanation for the step-wise addition of sugars to the GAG chain during biosynthesis was determined by analyzing mutants of the pmHAS enzyme. pmHAS possesses two independent catalytic sites in one polypeptide. Mutants were created that transferred only GlcUA, and distinct mutants were also created that transferred only GlcNAc. These mutants cannot polymerize HA chains individually, but if the two types of mutants are mixed together in the same reaction with an acceptor molecule, then polymerization was rescued. The chondroitin synthase, pmCS, has a similar sequence and similar two-domain structure. The heparosan synthases, pmHS1 and PmHS2, also contain regions for the two active sites. Single action mutants have also been created for the chondroitin synthase, pmCS, and are described hereinafter in detail.

[00099] The naturally occuring *Pasteurella* GAG synthases are very specific glycosyltransferases with respect to the sugar transfer reaction; only the correct monosaccharide from the authentic UDP-sugar is added onto acceptors. The epimers or other closely structurally related precursor molecules (e.g. UDP-glucose) are not utilized. The GAG synthases do, however, utilize certain heterologous acceptor sugars. For example, pmHAS will elongate short chondroitin acceptors with long HA chains. pmHS1 will also add long heparosan chains onto HA acceptor oligosaccharides as well as heparin oligosaccharides (see hereinbelow). Therefore, the presently claimed and disclosed invention encompasses a wide range of hybrid or chimeric GAG oligosaccharides prepared utilizing these *P. multocida* GAG catalysts.

[000100] As used herein, the term "nucleic acid segment" and "DNA segment" are used interchangeably and refer to a DNA molecule which has been isolated free of total genomic DNA of a particular species. Therefore, a "purified" DNA or nucleic acid segment as used herein, refers to a DNA segment which contains a Hyaluronate Synthase ("HAS") coding sequence or Chondroitin Synthase ("CS") coding sequence or Heparin/Heparosan Synthase ("HS") coding sequence yet is isolated away from, or purified free from, unrelated genomic DNA, for example, total *Pasteurella multocida*. Included within the term "DNA segment", are DNA segments and smaller fragments of such segments, and also recombinant vectors, including, for example, plasmids, cosmids, phage, viruses, and the like.

[000101] Similarly, a DNA segment comprising an isolated or purified *pmHAS or pmCS or pmHS1 or PmHS2* gene refers to a DNA segment including HAS or CS or HS coding sequences isolated substantially away from other naturally occurring genes or protein encoding sequences.

In this respect, the term "gene" is used for simplicity to refer to a functional protein-, polypeptide- or peptide- encoding unit. As will be understood by those in the art, this functional term includes genomic sequences, cDNA sequences or combinations thereof. "Isolated substantially away from other coding sequences" means that the gene of interest, in this case *pmHAS or pmCS or pmHS1 or PmHS2* forms the significant part of the coding region of the DNA segment, and that the DNA segment does not contain other non-relevant large portions of naturally-occurring coding DNA, such as large chromosomal fragments or other functional genes or DNA coding regions. Of course, this refers to the DNA segment as originally isolated, and does not exclude genes or coding regions later added to, or intentionally left in, the segment by the hand of man.

[000102] Due to certain advantages associated with the use of prokaryotic sources, one will likely realize the most advantages upon isolation of the HAS or CS or HS gene from the prokaryote *P. multocida*. One such advantage is that, typically, eukaryotic genes may require significant post-transcriptional modifications that can only be achieved in a eukaryotic host. This will tend to limit the applicability of any eukaryotic HAS or CS or HS gene that is obtained. Moreover, those of ordinary skill in the art will likely realize additional advantages in terms of time and ease of genetic manipulation where a prokaryotic enzyme gene is sought to be employed. These additional advantages include (a) the ease of isolation of a prokaryotic gene because of the relatively small size of the genome and, therefore, the reduced amount of screening of the corresponding genomic library and (b) the ease of manipulation because the overall size of the coding region of a prokaryotic gene is significantly smaller due to the absence of introns. Furthermore, if the product of the pmHAS or pmCS or pmHS1 or PmHS2 gene (i.e., the enzyme) requires posttranslational modifications, these would best be achieved in a similar prokaryotic cellular environment (host) from which the gene was derived.

[000103] Preferably, DNA sequences in accordance with the present invention will further include genetic control regions which allow the expression of the sequence in a selected recombinant host. The genetic control region may be native to the cell from which the gene was isolated, or may be native to the recombinant host cell, or may be an exaggerous segment that is compatible with and recognized by the transcriptional machinery of the selected recbominant host cell. Of course, the nature of the control region employed will generally vary depending on the particular use (e.g., cloning host) envisioned.

[000104] In particular embodiments, the invention concerns isolated DNA segments and recombinant vectors incorporating DNA sequences which encode a *pmHAS or pmCS or pmHS1 or PmHS2* gene, that includes within its amino acid sequence an amino acid sequence in accordance with SEQ ID NO:2, 4, 6, 8, 9, or 70, respectively. Moreover, in other particular

embodiments, the invention concerns isolated DNA segments and recombinant vectors incorporating DNA sequences which encode a gene that includes within its nucleic acid sequence an amino acid sequence encoding HAS or CS or HS pepetides or peptide fragment thereof, and in particular to a HAS or CS or HS peptide or peptide fragment thereof, corresponding to *Pasteurella multocida* HAS or CS or HS. For example, where the DNA segment or vector encodes a full length HAS or CS or HS protein, or is intended for use in expressing the HAS or CS or HS protein, preferred sequences are those which are essentially as set forth in SEQ ID NO:1, 3, 5, 7, 69, or 71, respectively.

[000105] Truncated *pmHAS* gene (such as, but not limited to, $pmHAS^{1-703}$, SEQ ID NO:71) also falls within the definition of preferred sequences as set forth above. For instance, at the carboxyl terminus, approximately 270-272 amino acids may be removed from the sequence and still have a functioning HAS. Those of ordinary skill in the art would appreciate that simple amino acid removal from either end of the pmHAS sequence can be accomplished. The truncated versions of the sequence (as disclosed hereinafter) simply have to be checked for HAS activity in order to determine if such a truncated sequence is still capable of producing HAS. The other GAG synthases disclosed and claimed herein are also amenable to truncation or alteration with preservation of activity and such truncated or alternated GAG synthases also fall within the scope of the present invention.

[000106] Nucleic acid segments having HAS or CS or HS activity may be isolated by the methods described herein. The term "a sequence essentially as set forth in SEQ ID NO:X" means that the sequence substantially corresponds to a portion of SEQ ID NO:X and has relatively few amino acids or codons encoding amino acids which are not identical to, or a biologically functional equivalent of, the amino acids or codons encoding amino acids of SEQ ID NO:X. The term "biologically functional equivalent" is well understood in the art and is further defined in detail herein, as a gene having a sequence essentially as set forth in SEQ ID NO:X, and that is associated with the ability of prokaryotes to produce HA or a hyaluronic acid or chondroitin or heparin polymer *in vitro* or *in vivo*. In the above examples "X" refers to either SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 69, 70 or 71 or any additional sequences set forth herein, such as the truncated or mutated versions of $pmHAS^{1-703}$ that are contained generally in SEQ ID NOS:10-60.

[000107] The art is replete with examples of practitioner's ability to make structural changes to a nucleic acid segment (i.e. encoding conserved or semi-conserved amino acid substitutions) and still preserve its enzymatic or functional activity when expressed. See for special example of literature attesting to such: (1) Risler et al. "Amino Acid Substitutions in Structurally Related Proteins. A Pattern Recognition Approach." J. Mol. Biol. 204:1019-1029

(1988) ["... according to the observed exchangeability of amino acid side chains, only four groups could be delineated; (I) Ile and Val; (ii) Leu and Met, (iii) Lys, Arg, and Gln, and (iv) Tyr and Phe."]; (2) Niefind et al. "Amino Acid Similarity Coefficients for Protein Modeling and Sequence Alignment Derived from Main-Chain Folding Anoles." J. Mol. Biol. 219:481-497 (1991) [similarity parameters allow amino acid substitutions to be designed]; and (3) Overington et al. "Environment-Specific Amino Acid Substitution Tables: Tertiary Templates and Prediction of Protein Folds," Protein Science 1:216-226 (1992) ["Analysis of the pattern of observed substitutions as a function of local environment shows that there are distinct patterns..." Compatible changes can be made.]

[000108] These references and countless others, indicate that one of ordinary skill in the art, given a nucleic acid sequence or an amino acid, could make substitutions and changes to the nucleic acid sequence without changing its functionality (specific examples of such changes are given hereinafter and are generally set forth in SEQ ID NOS:10-60). Also, a substituted nucleic acid segment may be highly identical and retain its enzymatic activity with regard to its unadulterated parent, and yet still fail to hybridize thereto. Additionally, the present application discloses 4 enzymes and numerous mutants of these enzymes that still retain at least 50% of the enzymatic activity of the unmutated parent enzyme – i.e. ½ of the dual action transferase activity of the unadulterated parent. As such, variations of the sequences and enzymes that fall within the above-defined functional limitations have been disclosed and enabled. One of ordinary skill in the art, given the present specification, would be able to identify, isolate, create, and test DNA sequences and/or enzymes that produce natural or chimeric or hybrid GAG molecules. As such, the presently claimed and disclosed invention should not be regarded as being solely limited to the specific sequences disclosed herein.

[000109] The invention discloses nucleic acid segments encoding an enzymatically active HAS or CS or HS from *P. multocida* - pmHAS, pmCS, pmHS1, and PmHS2, respectively. One of ordinary skill in the art would appreciate that substitutions can be made to the pmHAS or pmCS or pmHS1 or PmHS2 nucleic acid segments listed in SEQ ID NO:1, 3, 5, 7, 69, and 71, respectively, without deviating outside the scope and claims of the present invention. Indeed, such changes have been made and are described hereinafter with respect to the mutants produced. Standardized and accepted functionally equivalent amino acid substitutions are presented in Table II. In addition, other analogous or homologous enzymes that are functionally equivalent to the disclosed synthase sequences would also be appreciated by those skilled in the art to be similarly useful in the methods of the present invention, that is, a new method to control precisely the size distribution of polysaccharides, namely glycosaminoglycans.

TABLE II

Amin Acid Group	C nservative and Semi-Conservative Substitutions
NonPolar R Groups	Alanine, Valine, Leucine, Isoleucine, Proline, Methionine, Phenylalanine, Tryptophan
Polar, but uncharged, R Groups	Glycine, Serine, Threonine, Cysteine, Asparagine, Glutamine
Negatively Charged R Groups	Aspartic Acid, Glutamic Acid
Positively Charged R Groups	Lysine, Arginine, Histidine

[000110] Another preferred embodiment of the present invention is a purified nucleic acid segment that encodes a protein in accordance with SEQ ID NO:1 or 3 or 5 or 7 or 71, respectively, further defined as a recombinant vector. As used herein, the term "recombinant vector" refers to a vector that has been modified to contain a nucleic acid segment that encodes an HAS or CS or HS protein, or fragment thereof. The recombinant vector may be further defined as an expression vector comprising a promoter operatively linked to said HAS- or CS- or HS- encoding nucleic acid segment.

[000111] A further preferred embodiment of the present invention is a host cell, made recombinant with a recombinant vector comprising an HAS or CS or HS gene. The preferred recombinant host cell may be a prokaryotic cell. In another embodiment, the recombinant host cell is an eukaryotic cell. As used herein, the term "engineered" or "recombinant" cell is intended to refer to a cell into which a recombinant gene, such as a gene encoding HAS or CS or HS, has been introduced mechanically or by the hand of man. Therefore, engineered cells are distinguishable from naturally occurring cells which do not contain a recombinantly introduced gene. Engineered cells are thus cells having a gene or genes introduced through the hand of man. Recombinantly introduced genes will either be in the form of a cDNA gene, a copy of a genomic gene, or will include genes positioned adjacent to a promoter associated or not naturally associated with the particular introduced gene.

[000112] In preferred embodiments, the HAS- or CS- or HS- encoding DNA segments further include DNA sequences, known in the art functionally as origins of replication or "replicons", which allow replication of contiguous sequences by the particular host. Such origins allow the preparation of extrachromosomally localized and replicating chimeric or hybrid segments or plasmids, to which HAS- or CS- or HS- encoding DNA sequences are ligated. In

more preferred instances, the employed origin is one capable of replication in bacterial hosts suitable for biotechnology applications. However, for more versatility of cloned DNA segments, it may be desirable to alternatively or even additionally employ origins recognized by other host systems whose use is contemplated (such as in a shuttle vector).

[000113] The isolation and use of other replication origins such as the SV40, polyoma or bovine papilloma virus origins, which may be employed for cloning or expression in a number of higher organisms, are well known to those of ordinary skill in the art. In certain embodiments, the invention may thus be defined in terms of a recombinant transformation vector which includes the HAS- or CS- or HS- coding gene sequence together with an appropriate replication origin and under the control of selected control regions.

[000114] Thus, it will be appreciated by those of skill in the art that other means may be used to obtain the HAS or CS or HS gene or cDNA, in light of the present disclosure. For example, polymerase chain reaction or RT-PCR produced DNA fragments may be obtained which contain full complements of genes or cDNAs from a number of sources, including other strains of *Pasteurella* or from a prokaryot with similar glycosyltransferases or from eukaryotic sources, such as cDNA libraries. Virtually any molecular cloning approach may be employed for the generation of DNA fragments in accordance with the present invention. Thus, the only limitation generally on the particular method employed for DNA isolation is that the isolated nucleic acids should encode a biologically functional equivalent HAS or CS or HS.

[000115] Once the DNA has been isolated, it is ligated together with a selected vector. Virtually any cloning vector can be employed to realize advantages in accordance with the invention. Typical useful vectors include plasmids and phages for use in prokaryotic organisms and even viral vectors for use in eukaryotic organisms. Examples include pKK223-3, pSA3, recombinant lambda, SV40, polyoma, adenovirus, bovine papilloma virus and retroviruses. However, it is believed that particular advantages will ultimately be realized where vectors capable of replication in both biotechnologically useful Gram-positive or Gram-negative bacteria (e.g. *Bacillus*, *Lactococcus*, or *E. coli*) are employed.

[000116] Vectors such as these, exemplified by the pSA3 vector of Dao and Ferretti or the pAT19 vector of Trieu-Cuot, et al., allow one to perform clonal colony selection in an easily manipulated host such as *E. coli*, followed by subsequent transfer back into a food grade *Lactococcus* or *Bacillus* strain for production of hyaluronan or chondroitin or heparin polymer. In another embodiment, the recombinant vector is employed to make the functional GAG synthase for *in vitro* use. These are benign and well studied organisms used in the production of certain foods and biotechnology products and are recognized as GRAS (generally recognized as safe) organisms. These are advantageous in that one can augment the *Lactococcus* or

Bacillus strain's ability to synthesize HA or chondroitin or heparin through gene dosaging (i.e., providing extra copies of the HAS or CS or HS gene by amplification) and/or inclusion of additional genes to increase the availability of HA or chondroitin or heparin precursors. The inherent ability of a bacterium to synthesize HA or chondroitin or heparin can also be augmented through the formation of extra copies, or amplification, of the plasmid that carries the HAS or CS or HS gene. This amplification can account for up to a 10-fold increase in plasmid copy number and, therefore, the HAS or CS or HS gene copy number.

[000117] Another procedure to further augment HAS or CS or HS gene copy number is the insertion of multiple copies of the gene into the plasmid. Another technique would include integrating at least one copy of the HAS or CS or HS gene into chromosomal DNA. This extra amplification would be especially feasible, since the bacterial HAS or CS or HS gene size is small. In some scenarios, the chromosomal DNA-ligated vector is employed to transfect the host that is selected for clonal screening purposes such as *E. coli*, through the use of a vector that is capable of expressing the inserted DNA in the chosen host.

[000118] In certain other embodiments, the invention concerns isolated DNA segments and recombinant vectors that include within their sequence a nucleic acid sequence essentially as set forth in SEQ ID NO:1,3,5,7,69, or 71. The term "essentially as set forth" in SEQ ID NO: 1,3,5,7,69, or 71 is used in the same sense as described above and means that the nucleic acid sequence substantially corresponds to a portion of SEQ ID NO: 1,3,5,7,69, or 71 and has relatively few codons which are not identical, or functionally equivalent, to the codons of SEQ ID NO: 1,3,5,7,69, or 71. The term "functionally equivalent codon" is used herein to refer to codons that encode the same amino acid, such as the six codons for arginine or serine, and also refers to codons that encode biologically equivalent amino acids, as set forth in Table II.

[000119] It will also be understood that amino acid and nucleic acid sequences may include additional residues, such as additional N- or C-terminal amino acids or 5' or 3' nucleic acid sequences, and yet still be essentially as set forth in one of the sequences disclosed herein, so long as the sequence meets the criteria set forth above, including the maintenance of biological protein activity where protein expression and enzyme activity is concerned. The addition of terminal sequences particularly applies to nucleic acid sequences which may, for example, include various non-coding sequences flanking either of the 5' or 3' portions of the coding region or may include various internal sequences, which are known to occur within genes. Furthermore, residues may be removed from the N- or C-terminal amino acids and yet still be essentially as set forth in one of the sequences disclosed herein, so long as the sequence meets the criteria set forth above, as well.

[000120] Allowing for the degeneracy of the genetic code as well as conserved and semi-

conserved substitutions, sequences which have between about 40% and about 99%; or more preferably, between about 80% and about 90%; or even more preferably, between about 90% and about 99% identity to the nucleotides of SEQ ID NO: 1,3,5,7,69, or 71 will be sequences which are "essentially as set forth" in SEQ ID NO: 1,3,5,7,69, or 71. Sequences which are essentially the same as those set forth in SEQ ID NO: 1,3,5,7,69, or 71 may also be functionally defined as sequences which are capable of hybridizing to a nucleic acid segment containing the complement of SEQ ID NO: 1,3,5,7,69, or 71 under "standard stringent hybridization conditions," "moderately stringent hybridization conditions," "less stringent hybridization conditions," or "low stringency hybridization conditions." Suitable "standard" or "less stringent" hybridization conditions will be well known to those of skill in the art and are clearly set forth hereinbelow. In a preferred embodiment, standard stringent hybridization conditions or less stringent hybridization conditions are utilized.

[000121] The terms "standard stringent hybridization conditions," "moderately stringent conditions," and "less stringent hybridization conditions" or "low stringency hybridization conditions" are used herein, describe those conditions under which substantially complementary nucleic acid segments will form standard Watson-Crick base-pairing and thus "hybridize" to one another. A number of factors are known that determine the specificity of binding or hybridization, such as pH; temperature; salt concentration; the presence of agents, such as formamide and dimethyl sulfoxide; the length of the segments that are hybridizing; and the like. There are various protocols for standard hybridization experiments. Depending on the relative similarity of the target DNA and the probe or query DNA, then the hybridization is performed under stringent, moderate, or under low or less stringent conditions.

[000122] The hybridizing portion of the hybridizing nucleic acids is typically at least about 14 nucleotides in length, and preferably between about 14 and about 100 nucleotides in length. The hybridizing portion of the hybridizing nucleic acid is at least about 60%, e.g., at least about 80% or at least about 90%, identical to a portion or all of a nucleic acid sequence encoding a HAS or chondroitin or heparin synthase or its complement, such as SEQ ID NO: 1,3,5,7,69, or 71 or the complement thereof. Hybridization of the oligonucleotide probe to a nucleic acid sample typically is performed under standard or stringent hybridization conditions. Nucleic acid duplex or hybrid stability is expressed as the melting temperature or T_m, which is the temperature at which a probe nucleic acid sequence dissociates from a target DNA. This melting temperature is used to define the required stringency conditions. If sequences are to be identified that are related and substantially identical to the probe, rather than identical, then it is useful to first establish the lowest temperature at which only homologous hybridization occurs with a particular concentration of salt (e.g., SSC, SSPE, or HPB). Then, assuming that

1% mismatching results in a 1°C decrease in the T_m, the temperature of the final wash in the hybridization reaction is reduced accordingly (for example, if sequences having >95% identity with the probe are sought, the final wash temperature is decreased by about 5°C). In practice, the change in T_m can be between about 0.5°C and about 1.5°C per 1% mismatch. Examples of standard stringent hybridization conditions include hybridizing at about 68°C in 5x SSC/5x Denhardt's solution/1.0% SDS, followed with washing in 0.2x SSC/0.1% SDS at room temperature or hybridizing in 1.8xHPB at about 30°C to about 45°C followed by washing a 0.2-0.5xHPB at about 45°C. Moderately stringent conditions include hybridizing as described above in 5xSSC\5xDenhardt's solution 1% SDS washing in 3x SSC at 42°C. The parameters of salt concentration and temperature can be varied to achieve the optimal level of identity between the probe and the target nucleic acid. Additional guidance regarding such conditions is readily available in the art, for example, by Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, (Cold Spring Harbor Press, N.Y.); and Ausubel et al. (eds.), 1995, Current Protocols in Molecular Biology, (John Wiley & Sons, N.Y.). Several examples of low stringency protocols include: (A) hybridizing in 5X SSC, 5X Denhardts reagent, 30% formamide at about 30°C for about 20 hours followed by washing twice in 2X SSC,0.1% SDS at about 30°C for about 15 min followed by 0.5X SSC, 0.1% SDS at about 30°C for about 30 min (FEMS Microbiology Letters, 2000, vol. 193, p. 99-103); (B) hybridizing in 5X SSC at about 45°C overnight followed by washing with 2X SSC, then by 0.7X SSC at about 55°C. (J. Viological Methods, 1990, vol. 30, p. 141-150); or (C) hybridizing in 1.8XHPB at about 30°C to about 45°C; followed by washing in 1X HPB at 23°C.

[000123] Naturally, the present invention also encompasses DNA segments which are complementary, or essentially complementary, to the sequences set forth in SEQ ID NO:1 or 3 or 5 or 7 or 69 or 71. Nucleic acid sequences which are "complementary" are those which are capable of base-pairing according to the standard Watson-Crick complementarity rules. For example, the sequence 5'-ATAGCG-3' is complementary to the sequence 5'-CGCTAT-3" because when the two sequences are aligned, each "T" is able to base-pair with an "A", which each "G" is able to base pair with a "C". As used herein, the term "complementary sequences" means nucleic acid sequences which are substantially complementary, as may be assessed by the nucleotide comparison set forth above, or as defined as being capable of hybridizing to the nucleic acid segment of SEQ ID NO: 1,3,5,7, or 69, or 71 under standard stringent, moderately stringent, or less stringent hybridizing conditions.

[000124] The nucleic acid segments of the present invention, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, epitope tags,

polyhistidine regions, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol.

[000125] Naturally, it will also be understood that this invention is not limited to the particular amino acid and nucleic acid sequences of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 69, 70, or 71. Recombinant vectors and isolated DNA segments may therefore variously include the HAS or CS or HS coding regions themselves, coding regions bearing selected alterations or modifications in the basic coding region, or they may encode larger polypeptides which nevertheless include HAS or CS or HS coding regions or may encode biologically functional equivalent proteins or peptides which have variant amino acid sequences.

[000126] The DNA segments of the present invention encompass DNA segments encoding biologically functional equivalent HAS or CS or HS proteins and peptides. Such sequences may arise as a consequence of codon redundancy and functional equivalency which are known to occur naturally within nucleic acid sequences and the proteins thus encoded. Alternatively, functionally equivalent proteins or peptides may be created via the application of recombinant DNA technology, in which changes in the protein structure may be engineered, based on considerations of the properties of the amino acids being exchanged. Changes designed by man may be introduced through the application of site-directed mutagenesis techniques, e.g., to introduce improvements to the enzyme activity or to antigenicity of the HAS or CS or HS protein or to test HAS or CS or HS mutants in order to examine HAS or CS or HS activity at the molecular level or to produce HAS or CS or HS mutants having changed or novel enzymatic activity and/or sugar substrate specificity.

[000127] Traditionally, chemical or physical treatments of polysaccharides were required to join two dissimilar materials. For example, a reactive nucleophile group of one polymer or surface was exposed to an activated acceptor group of the other material. Two main problems exist with this approach, however. First, the control of the chemical reaction cannot be refined, and differences in temperature and level of activation often result in a distribution of several final products that vary from lot to lot preparation. For instance, several chains may be cross-linked in a few random, ill-defined areas, and the resulting sample is not homogenous. Second, the use of chemical reactions to join molecules often leaves an unnatural or nonbiological residue at the junction of biomaterials. For example, the use of an amine and an activated carboxyl group would result in an amide linkage. This inappropriate residue buried in a carbohydrate may pose problems with biological systems such as the subsequent production of degradation products which accumulate to toxic levels or the triggering of an immune

response.

Use of pmHAS for Polymer Grafting and Polysaccharide Production.

[000128] Most polysaccharide polymers must be of a certain length before their physical or biological properties become apparent. Often the polysaccharide must comprise at least 20-100 sugar units. Certain enzymes that react with exogenous polymers have been previously available, but typically add only one sugar unit. The unique enzymes described in the present invention, (e.g. pmHAS, pmCS, pmHS1, and PmHS2) form polymers of at least 100-400 sugar units in length. Thus, one embodiment of the presently claimed and disclosed invention, results in long, defined linear polymers composed of only natural glycosidic linkages.

[000129] The four known glycosaminoglycan synthesizing enzymes from *Pasteurella multocida* bacteria normally make polymers similar to or identical to vertebrate polymers. These bacteria employ the polysaccharide, either HA (Type A bacteria), chondroitin (Type F bacteria), or heparosan (unsulfated, unepimerized heparin - Type D bacteria) as an extracellular coating to serve as molecular camouflage. Native enzymes normally make polymer chains of a single type of sugar repeat. If a recombinant HAS or CS or HS enzyme is employed, however, the enzyme can be forced to work on an exogenous functional acceptor molecule. For instance, the recombinant enzyme may be incubated with a polymer acceptor, and the recombinant enzyme will then elongate the acceptor with UDP-sugar precursors. The known native enzymes do not perform this reaction since they already contain a growing polymer chain that was formed in the living cell; enzyme preparations from native cells retain the polymer following isolation.

[000130] pmHAS (SEQ ID NO:2), a 972 amino acid residue protein from *Pasteurella multocida*, is made in a functional state in recombinant *Escherichia coli*. The *pmHAS* gene is given in SEQ ID NO:1. Other functional derivatives of pmHAS, for example an enzyme called $pmHAS^{1-703}$ (SEQ ID NO:9) and the $pmHAS^{1-703}$ gene (SEQ ID NO:71), have been produced which are soluble. The soluble form can be prepared in larger quantities and in a purer state than the naturally occurring full-length enzyme. The preferred *E. coli* strains do not have an UDP-Glc dehydrogenase and therefore the recombinant enzyme does not make HA chain in the foreign host. Therefore, the enzyme is in a "virgin" state since the empty acceptor site can be occupied with foreign polymers. For example, the recombinant enzyme may be incubated in a mixture comprising from about 10 to about 50mM Tris pH 7.2, from 0.5 to about 20 mM $MnCl_2$, from about 0.1 to about 30 mM UDP-GlcUA, from about 0.1 to about 30 mM UDP-GlcNAc, and a suitable acceptor at about 20-37°C for from about 1 to about 600 minutes.

Suitable acceptors can be any functional acceptor, such as a glycosaminoglycan acceptor or sugar acceptor, for example, but not by limitation, short HA chains (two or more sugar units such as HA_4) or short chondroitin sulfate chains (5 sugar units) or long chondroitin sulfate chains ($\sim 10^2$ sugar units). In the case of the latter acceptors, pmHAS (or its derivatives), then elongates the foreign acceptors (i.e. long or short chondroitin polymers) at their nonreducing termini with authentic HA chains. The length of the HA chain added onto the acceptor is controlled by altering the concentration of UDP-sugars (thus changing the stoichiometry of UDP-sugar to acceptor) and/or the reaction time. Immobilized acceptors, such as beads or other solid objects with bound acceptor oligosaccharides, can also be extended by the pmHAS enzyme using UDP-sugars. In this manner, the pmHAS enzyme (or its derivatives) can be used to attach polysaccharide chains to any suitable acceptor molecule.

[000131] Type A *P. multocida* produces HA capsule [GlcUA-GlcNAc repeats] and possesses the pmHAS enzyme. On the other hand, Type F *P. multocida* produces a chondroitin or chondroitin-like polymer capsule [GlcUA-GalNAc repeats]. The DNA encoding an open reading frame (GenBank accession #AF195517) that is 90% identical to pmHAS at the protein level has been cloned; this enzyme is called PmCS, the *P. multocida* chondroitin synthase. The amino acid sequence of pmCS is set forth in Seq ID NO: 4 and the *pmCS* gene sequence is set forth in SEQ ID NO: 3. As the PmCS enzyme's sequence is so similar to pmHAS, one of ordinary skill in the art, given the present specification, is able to manipulate the pmCS in the same manner as that for pmHAS and any manipulation that is successful with regard to the pmHAS would be performable with the pmCS, with the exception that chondroitin chains would be grafted instead of HA. Either HA or chondroitin or heparin chains can serve as acceptors for pmCS as both acceptors serve well for pmHAS.

[000132] Such hybrid polysaccharide materials composed of HA, chondroitin and heparin cannot be formed in a controlled fashion (targeted size and monodisperse) especially with regard to medium to large size polymers (i.e. greater than 15KDa) by any other existing process without (1) leaving unnatural residues and/or (2) producing undesirable crosslinking reactions. The testicular hyaluronidase method gives a variety of small products derived from quasi-random linkage of GAGs, HA and chondroitin. Very large polymers are not major or significant products. The chimeric or hybrid polysaccharide materials can serve as a biocompatible molecular glue for cell/cell interactions in artificial tissues or organs and the HA/chondroitin/heparin hybrid mimics natural proteoglycans that normally contain an additional protein intermediate between polymer chains. The present invention, therefore, obviates the requirement for a protein intermediary. A recombinant HA/chondroitin/heparin chimeric or hybrid polysaccharide, devoid of such an intermediary protein, is desirous since molecules from

animal sources are potentially immunogenic -- the chimeric or hybrid polysaccharide, however, would not appear as "foreign" to the host, thus no immune response is generated. Also, the recombinant polymers can be made free of adventitious agents (e.g. prions, viruses etc.)

[000133] An intrinsic and essential feature of polysaccharide synthesis is the repetitive addition of sugar monomer units to the growing polymer. The glycosyltransferase remains in association with the nascent chain. This feature is particularly relevant for HA biosynthesis as the HA polysaccharide product, in all known cases, is transported out of the cell; if the polymer was released, then the HAS would not have another chance to elongate that particular molecule. Three possible mechanisms for maintaining the growing polymer chain at the active site of the enzyme are immediately obvious. First, the enzyme possesses a carbohydrate polymer binding pocket or cleft. Second, the nascent chain is covalently attached to the enzyme during its synthesis. Third, the enzyme binds to the nucleotide base or the lipid moiety of the precursor while the nascent polymer chain is still covalently attached.

[000134] The HAS activity of the native pmHAS enzyme found in *P. multocida* membrane preparations is not stimulated by the addition of HA oligosaccharides; theoretically, the endogenous nascent HA chain initiated *in vivo* renders the exogenously supplied acceptor unnecessary. However, recombinant pmHAS produced in an *E. coli* strain that lacks the UDP-GlcUA precursor, and thus lacks a nascent HA chain, is able to bind and to elongate exogenous HA oligosaccharides. As mentioned above, there are three likely means for a nascent HA chain to be held at or near the active site. In the case of pmHAS, it appears that a HA-binding site exists near or at the sugar transferase catalytic site.

[000135] Defined oligosaccharides that vary in size and composition are used to discern the nature of the interaction between pmHAS and the sugar chain. For example, it appears that the putative HA-polymer binding pocket of pmHAS will bind and elongate at least an intact HA disaccharide with increased efficiency occurring when a trisaccharide is used (reduced tetramer or a synthetic trisaccharide). Oligosaccharide binding to pmHAS appears to be somewhat selective because the heparosan pentamer, which only differs in the glycosidic linkages from HA-derived oligosaccharides, does not serve as an acceptor. However, chondroitin [GlcUA-GalNAc repeat] does serve as an acceptor for pmHAS.

[000136] To date, no other HA synthase besides pmHAS has been shown to utilize an exogenous acceptor or primer sugar. In an early study of a cell-free HA synthesis system, preparations of native Group A *Streptococcal* HAS were neither inhibited nor stimulated by the addition of various HA oligosaccharides including the HA tetramer derived from testicular hyaluronidase digests. These membrane preparations were isolated from cultures that were producing copious amounts of HA polysaccharide. The cells were hyaluronidase-treated to

facilitate handling. Therefore, it is quite likely that the native streptococcal enzyme was isolated with a small nascent HA chain attached to or bound to the protein much as suspected in the case of the native pmHAS. Theoretically, the existing nascent chain formed *in vivo* would block the entry and subsequent utilization of an exogenous acceptor by the isolated enzyme *in vitro*. With the advent of molecularly cloned HAS genes, it is possible to prepare virgin enzymes lacking a nascent HA chain if the proper host is utilized for expression. In these tests, recombinant yeast with spHAS did not use HA acceptors proving that the Class I enzyme intrinsically cannot elongate such acceptors.

[000137] Both heparin and chondroitin, in mammalian systems, are synthesized by the addition of sugar units to the nonreducing end of the polymer chain. In vivo, the glycosyltransferases initiate chain elongation on at least primer monosachharides [more preferably tetrasaccharides such as xylose-galactose-galactose-GlcUA] that are attached to serine residues of proteoglycan core molecules. *In vitro*, enzyme extracts transfer a single sugar to exogenously added heparin or chondroitin oligosaccharides; unfortunately, the subsequent sugar of the disaccharide unit is usually not added and processive elongation to longer polymers does not occur. Therefore it is likely that some component is altered or missing in the *in vitro* system. In the case of heparin biosynthesis, a single enzyme transfers both GlcUA and GlcNAc sugars to the glycosaminoglycan chain based on co-purification or expression studies.

[000138] Recent work with the *E. coli* K5 KfiA and KfiC enzymes, which polymerize heparosan, indicates that a pair of proteins can transfer both sugars to the nonreducing end of acceptor molecules *in vitro*. Processive elongation, however, was not demonstrated in these experiments; crude cell lysates transferred a single sugar to defined even- or odd-numbered oligosaccharides.

[000139] Recombinant pmHAS adds single monosaccharides in a sequential fashion to the nonreducing termini of the nascent HA chain. Elongation of HA polymers containing hundreds of sugars has been demonstrated *in vitro*. The simultaneous formation of the disaccharide repeat unit is not necessary for generating the alternating structure of the HA molecule. The intrinsic specificity and fidelity of each half-reaction (e.g. GlcUA added to a GlcNAc residue or vice versa) apparently is sufficient to synthesize authentic HA chains.

[000140] A great technical benefit resulting from the alternating disaccharide structure of HA is that the reaction can be dissected by controlling the availability of UDP-sugar nucleotides. By omitting or supplying precursors in a reaction mixture, the glycosyltransferase may be stopped and started at different stages of synthesis of the heteropolysaccharide. In contrast, there is no facile way to control in a step-wise fashion the glycosyltransferase enzymes that

produce important homopolysaccharides such as chitin, cellulose, starch, and glycogen.

[000141] An alternative method for controlling polymerization has been accomplished by creating mutants that only add one sugar linkage onto a short HA oligosaccharide. For example, pmHAS$^{1-650}$ (SEQ. ID NO: 10) can only add single GlcNAc sugars onto the non-reducing end (i.e. HA tetrasaccharide [GlcNAc-GlcUA-GlcNAc-GlcUA]) of an acceptor (i.e. forms the HA pentamer). On the other hand, a mutant has been created and called pmHAS$^{1-703}$-D477N (SEQ. ID NO: 11) [pmHAS residues 1-703 with an asparagine substituted for the asparatate at position 477], that transfers only a single GlcNAc residue onto the non-reducing terminal GlcUa group of the short HA oligosaccharide. If extracts of two such single-action point mutants (e.g. D477N, SEQ ID NO:11 and D196N [i.e. pmHAS residues 1-703 with an asparagine sustituted for the aspartate at position 196], SEQ ID NO:12) are mixed together with an acceptor in the presence of UDP-GlcNAc and UDP-GlcUA, then significant polymerization is achieved. It is also obvious that by carrying out the steps of GlcNAc or GlcUA transfer separately and sequentially, almost any HA chain length is possible. The same is also true with regard to PmCS either alone or in combination with pmHAS as well as pmHS1 or PmHS2 either alone or in combination with pmCS and pmHAS, individually or as a group.

[000142] As stated above, membrane preparations from recombinant *E. coli* containing a pmHAS protein had HA synthase activity as judged by incorporation of radiolabel from UDP-[^{14}C]GlcUA into polymer when co-incubated with both UDP-GlcNAc and Mn ion. Due to the similarity at the amino acid level of pmHAS to several lipopolysaccharide transferases, it was hypothesized that HA oligosaccharides serve as acceptors for GlcUA and GlcNAc transfer. Addition of unlabeled even-numbered HA tetramer (from testicular hyaluronidase digests) to reaction mixtures with recombinant pmHAS$^{1-703}$ stimulates incorporation of radiolabel from UDP-[^{14}C]GlcUA into HA polymer by ~20- to 60-fold in comparison to reactions without oligosaccharides as shown in FIG. 1. The acceleration of incorporation by acceptor was not predicted or expected. The mechanism of action is probably the bypassing of a slow polymer initiation step; the synthase with acceptor proceeds rapidly to the fast elongation step. The present invention builds on these kinetic observations in reactions set up by the hand of man with recombinant versions of the

[000143] In FIG. 1, a series of reactions containing pmHAS$^{1-703}$ (30 μg total membrane protein) were incubated with UDP-[^{14}C]GlcUA (2x10^4 dpm, 120 μM) and UDP-GlcNAc (450 μM) in assay buffer (50 μl reaction vol) in the presence of no added sugar (none) or various oligosaccharides (HA4, 4 μg HA tetramer; unsHA4/6, 4 μg unsaturated HA "tetramer" and "hexamer"; chito4, 50 μg chitotetraose; hep5, 20 μg heparosan pentamer). After 1 hour, the reactions were analyzed by descending paper chromatography. Incorporation of radiolabel from

UDP-[^{14}C]GlcUA into high molecular weight HA is shown. The intact tetramer (HA4) served as a functional acceptor. Reactions with heparosan and chitooligosaccharides, as well as GlcNAc and/or GlcUA (not shown), incorporated as much radiolabel as parallel reactions with no acceptor. The free monosaccharides GlcUA and GlcNAc, either singly or in combination at concentrations of up to 100 μM, do not serve as acceptors; likewise, the beta-methyl glycosides of these sugars do not stimulate HAS activity.

[000144] In the same manner, pmHAS$^{1-703}$ has been shown to add sugars onto a chondroitin pentamer acceptor. The pmHAS$^{1-703}$ and reagents were prepared in the same manner as shown in Fig.1, except that a chondroitin pentamer was used as the acceptor molecule. The results of this experiment are shown in TABLE III.

TABLE III

Sugar	Mass	Incorporation of ^{14}C-GlcUA dpm
None	Not Applicable.	60
HA	5 µg	2,390
Chondroitin Pentamer	20 µg	6,690

[000145] Thus, it can be seen that the pmHAS$^{1-703}$ can utilize molecules other than the naturally occurring acceptors or primer molecules as the basis for forming a polysaccharide polymer chain.

[000146] The HA polymerizing activity of recombinant pmHAS$^{1-703}$ is dependent on the simultaneous incubation with both UDP-sugar precursors and a Mn^{2+} ion. The level of incorporation is dependent on protein concentration, on HA oligosaccharide concentration, and on incubation time as shown in FIG. 2. In FIG. 2, two parallel reactions containing pmHAS$^{1-703}$ with even-numbered HA oligosaccharides (105 μg membrane protein/point with a mixture of HA hexamer, octamer, and decamer, 4.4. μg total; solid circles) or six-fold more pmHAS$^{1-703}$ without oligosaccharide acceptor (630 μg protein/point; open circles) were compared. The enzyme preparations were added to prewarmed reaction mixtures containing UDP-[^{14}C]GlcUA (240 μM 6 x 10^4 dpm/point) and UDP-GlcNAc (600 μM) in assay buffer. At various times, 50 μl aliquots were withdrawn, terminated, and analyzed by paper chromatography. The exogenously supplied acceptor accelerated the bulk incorporation of sugar precursor into polymer product by pmHAS$^{1-703}$, but the acceptor was not absolutely required.

[000147] HA synthesized in the presence or the absence of HA oligosaccharides is sensitive to HA lyase (>95% destroyed) and has a molecular weight of ~1-5x10^4 Da (~50-250

monosaccharides). No requirement for a lipid-linked intermediate was observed as neither bacitracin (0.5 mg/ml) nor tunicamycin (0.2 mg/ml) alter the level of incorporation in comparison to parallel reactions with no inhibitor.

[000148] Gel filtration chromatography analysis of reactions containing recombinant pmHAS$^{1-703}$, ^{3}H-HA tetramer, UDP-GlcNAc and UDP-GlcUA show that labeled polymers from ~0.5 to 5x10^{4} Da (25-250 monosaccharides) are made as shown in FIG. 3. In FIG. 3, gel filtration analysis on Sephacryl S-200 (20 ml column, 0.7 ml fractions) shows that pmHAS$^{1-703}$ makes HA polysaccharide using HA tetramer acceptor and UDP-sugars. Dextrans of greater than or equal to 80 kDa (~400 monosaccharides) elute in the void volume (Vo arrow). The starting tetramer elutes in the included volume (Vi arrow). Membranes (190 μg total protein), UDP-GlcUA (200 μM), UDP-GlcNAc (600 μM), and radiolabeled ^{3}H-HA tetramer (1.1 x 10^{5} dpm) were incubated for 3 hours before gel filtration (solid squares). As a negative control, a parallel reaction containing all the components except for UDP-GlcNAc was analyzed (open squares). The small primer was elongated into higher molecular weight product if both precursors were supplied. In a parallel reaction without UDP-GlcNAc, the elution profile of the labeled tetramer is not altered.

[000149] The activity of the native pmHAS$^{1-703}$ from *P. multocida* membranes, however, is not stimulated by the addition of HA oligosaccharides under similar conditions. The native pmHAS$^{1-703}$ enzyme has an attached or bound nascent HA chain that is initiated in the bacterium prior to membrane isolation. The recombinant enzyme, on the other hand, lacks such a nascent HA chain since the *E. coli* host does not produce the UDP-GlcUA precursor needed to make HA polysaccharide. Therefore, the exogenous HA-derived oligosaccharide has access to the active site of pmHAS$^{1-703}$ and can be elongated.

[000150] The tetramer from bovine testicular hyaluronidase digests of HA terminates at the nonreducing end with a GlcUA residue and this molecule served as an acceptor for HA elongation by pmHAS$^{1-703}$. On the other hand, the tetramer and hexamer oligosaccharides produced by the action of *Streptomyces* HA lyase did not stimulate HA polymerization as shown in FIG. 1; "unsHA4/6". As a result of the lyase eliminative cleavage, the terminal unsaturated sugar is missing the C4 hydroxyl of GlcUA which would normally be extended by the HA synthase. The lack of subsequent polymerization onto this terminal unsaturated sugar is analogous to the case of dideoxynucleotides causing chain termination if present during DNA synthesis. A closed pyranose ring at the reducing terminus was not required by pmHAS$^{1-703}$ since reduction with borohydride did not affect the HA tetramer's ability to serve as an acceptor thus allowing the use of borotritide labeling to monitor the fate of oligosaccharides.

[000151] Neither Yeast-derived recombinant Group A HasA (spHAS) nor recombinant DG42

produced elongated HA-derived oligosaccharides into larger polymers. First, the addition of HA tetramer (or a series of longer oligosaccharides) did not significantly stimulate nor inhibit the incorporation of radiolabeled UDP-sugar precursors into HA (<5% of control value) by these Class I HA synthases. In parallel experiments, the HAS activity of HasA or DG42 was not affected by the addition of chitin-derived oligosaccharides. Second, the recombinant Class I enzymes did not elongate the radiolabeled HA tetramer in the presence of UDP-sugars (Table IV). These same preparations of enzymes, however, were highly active in the conventional HAS assay in which radiolabeled UDP-sugars were polymerized into HA.

TABLE IV

Enzyme	Units[a]	EDTA	Incorporation of HA4 into polymer (pmoles)
$PmHAS^{1-703}$	**6[b]**	**-**	**240**
		+	**1.7**
HasA	**9,800**	**-**	**≤0.2**
		+	**≤0.2**
DG42	**11,500**	**-**	**≤0.1**
		+	**≤0.3**

a - pmoles of GlcUA transfer/hr in the conventional HAS assay
b- measured without HA tetramer; 360 units with 100 μM HA tetramer.

[000152] As shown in Table IV, the various recombinant enzymes were tested for their ability to convert HA tetramer into molecular weight products. The reactions contained radiolabeled HA tetramer (5-8 x 10^5 dpm), 750 μM UDP-GlcNAc, 360 μM UDP-GlcUA, 20 mM XCl_2, 50 mM Tris, pH 7-7.6 (the respective X cation and pH values used for each enzyme were: $pmHAS^{1-703}$, Mn/7.2; *Xenopous* DG42, Mg/7.6; Group A *streptococcal* HasA, Mg/7.0), and enzyme (units/reaction listed). As a control, parallel reactions in which the metal ion was chelated (22 mM ethylenediaminetetraacetic acid final; EDTA column, rows with +) were tested; without free metal ion, the HAS enzymes do not catalyze polymerization. After 1 hour incubation, the reactions were terminated and subjected to descending paper chromatography. Only $pmHAS^{1-703}$ could elongate HA tetramer even though all three membrane preparations were very active in the conventional HAS assay (incorporation of [^{14}C]GlcUA from UDP-GlcUA into polymer when supplied UDP-GlcNAc).

[000153] Thin layer chromatography was utilized to monitor the pmHAS-catalyzed elongation reactions containing ^{3}H-labeled oligosaccharides and various combinations of UDP-sugar nucleotides. FIG. 4 demonstrates that pmHAS$^{1-703}$ elongated the HA-derived tetramer by a single sugar unit if the next appropriate UDP-sugar precursor was available in the reaction mixture. GlcNAc derived from UDP-GlcNAc was added onto the GlcUA residue at the nonreducing terminus of the tetramer acceptor to form a pentamer. On the other hand, inclusion of only UDP-GlcUA did not alter the mobility of the oligosaccharide. If both HA precursors are supplied, various longer products are made. In parallel reactions, control membranes prepared from host cells with a vector plasmid did not alter the mobility of the radiolabeled HA tetramer under any circumstances. In similar analyses monitored by TLC, pmHAS$^{1-703}$ did not utilize labeled chitopentaose as an acceptor.

[000154] As shown in FIG. 4, pmHAS extended an HA tetramer. In FIG. 4, radiolabeled HA tetramer (HA4 8x10^3 dpm ^{3}H) with a GlcUA at the nonreducing terminus was incubated with various combinations of UDP-sugars (A, 360 μM UDP-GlcUA; N, 750 μM UDP-GlcNAc; 0, no UDP-sugar), and pmHAS (55 μg membrane protein) in assay buffer for 60 minutes. The reactions (7 μl total) were terminated by heating at 95°C for 1 minute and clarified by centrifugation. Portions (2.5 μl) of the supernatant were spotted onto the application zone of a silica TLC plate and developed with solvent (1.25:1:1 butanol/acetic acid/water). The beginning of the analytical layer is marked by an arrow. The positions of odd-numbered HA oligosaccharides (S lane) are marked as number of monosaccharide units. The autoradiogram of FIG. 4 (4 day exposure) shows the single addition of a GlcNAc sugar onto the HA tetramer acceptor to form a pentamer when only the subsequent precursor is supplied (N). The mobility of the labeled tetramer is unchanged if only the inappropriate precursor, UDP-GlcUA (A), or no UDP-sugar (0) is present. If both UDP-sugars are supplied, then a ladder of products with sizes of 5, 7, 9, 11, and 13 sugars is formed (+AN). In a parallel experiment, chitopentaose (8 x 10^4 dpm ^{3}H) was tested as an acceptor substrate. Under no condition was this structurally related molecule extended by pmHAS.

[000155] HA-derived oligosaccharides with either GlcUA or GlcNAc at the nonreducing terminus served as acceptors for pmHAS$^{1-703}$ (FIG. 5). In FIG. 5, radiolabeled HA pentamer (HA5, 5x10^3 dpm ^{3}H) or HA tetramer (HA4, 25x10^3 dpm ^{3}H) was incubated with pmHAS$^{1-703}$ and various combinations of UDP-sugars (as in FIG. 4) for 2 or 20 minutes. Portions (1.5 μl) of the supernatant were spotted onto the TLC plate and developed in 1.5:1:1 solvent. This autoradiogram (1 mo. exposure) shows the single addition of a sugar onto an acceptor when only the appropriate precursor is supplied (HA4, N lane and HA5, A lane). If both UDP-sugars are supplied (+AN lanes), then a ladder of products with final sizes of 6, 8, and 10 sugars is

formed from either HA4 or HA5 in 2 minutes. After 20 minutes, a range of odd- and even-numbered product sugars are observed in reactions with HA4 and both UDP-sugars. In the 20 minute reaction with HA5 and both UDP-sugars, the HA products are so large that they do not migrate from the application zone.

[000156] Within two minutes, 2 to 6 sugar units were added, and after 20 minutes, at least of from about 9 to about 15 sugar units were added. In the experiments with the HA tetramer and both sugars, a ladder of even- and odd-numbered products is produced at the 20 minute time point. Therefore, in combination with the results of the single UDP-sugar experiments, the $pmHAS^{1-703}$ enzyme transfers individual monosaccharides sequentially during a polymerization reaction.

[000157] A series of truncated versions of pmHAS (normally a 972-residue membrane protein) were created and are tabulated (with functionality) in Table V that produce proteins with altered physical properties (i.e. proteins that are more conducive to high-level expression and purification) and altered function (i.e. single transferase activity). Polymerase chain reaction [PCR] was used to amplify a portion of the pmHAS gene using a primer corresponding to the authentic N-terminus sequence and a primer corresponding to an internal coding region which ended in a stop codon. The coding regions for the truncated proteins were cloned into an *Escherichia coli* expression plasmid (pKK223-3; Pharmacia) under control of the *tac* promoter. The DNA sequence was verified by automated sequencing.

[000158] The truncation series was generated and tested for activity. All proteins were made at the expected molecular weight, but not all proteins were active.

TABLE V

Name	Residues of pmHAS-D	Activity	SEQ ID NO:
$pmHAS^{437-972}$	437-972	N.D.	13
$pmHAS^{437-756}$	437-756	N.D.	14
$pmHAS^{1-756}$	1-756	HA Synthase	20
$pmHAS^{1-703}$	1-703	HA Synthase	9, 71
$pmHAS^{1-650}$	1-650	GlcNAc Transferase	10
$pmHAS^{152-756}$	152-756	N.D.	15

N.D. - no activity detected.

[000159] Analysis of induced cell cultures containing the plasmid with a 703-residue open reading frame revealed that a new 80-kDa protein, named $pmHAS^{1-703}$, was produced in large quantities. Furthermore, functional $pmHAS^{1-703}$ was present in the soluble fraction of the cell

lysate; thus allowing for rapid extraction and assay of the enzyme. pmHAS$^{1-703}$ was purified by sequential chromatography steps shown in FIG. 6. In FIG. 6, a soluble, active form of the HA synthase was constructed with molecular biological techniques. The recombinant enzyme from *E. coli* was purified by conventional chromatography with yields of up to 20 mg/liter of cell culture. FIG. 6 is a stained electrophoretic gel loaded with samples of pmHAS$^{1-703}$ (marked with an arrow) during different stages of chromatography. This catalyst (and improved mutant versions) can be used to prepare HA coatings on artificial surfaces or HA extensions on suitable acceptor molecules.

[000160] The pmHAS$^{1-703}$ is highly active and at least 95% pure as assessed by denaturing polyacrylamide gel electrophoresis. Mass spectrometric analysis indicates that the pmHAS$^{1-703}$ is the desired protein due to the close agreement of the calculated and the observed mass values. A buffer system has also been developed to stabilize the enzymatic activity in the range of 0° to 37°C.

[000161] Site-directed mutagenesis was then used to prepare versions of pmHAS$^{1-703}$ with altered enzymatic activity. Synthetic DNA oligonucleotides and multiple rounds of extension with *Pfu* DNA polymerase were used to add mutations to the coding region using the Quick-Change system from Stratagene. Through use of primers with mixed bases at certain positions, a wide variety of amino acid changes were generated. DNA sequencing was then employed to identify the changed residue. Several pmHAS$^{1-703}$ mutants have also been obtained having altered sugar transferase activity. Similar methodology has also been used to alter the HA-acceptor binding site of pmHAS$^{1-703}$.

[000162] Two positions of the pmHAS$^{1-703}$ sequence were mutated in the initial trials. Conserved aspartates at residue 196 or 477 were critical for HAS activity. Results are shown in Table VI.

TABLE VI

Mutation (*)	HAS Activity	GlcNActase	GlcUAtase	SEQ ID NO:
D196E	W/O	W/O	YES	16
D196N	W/O	W/O	YES	12
D196K	W/O	W/O	YES	17
D477E	W/O	YES	W/O	18
D477N	W/O	YES	W/O	11
D477K	W/O	YES	W/O	19
WILD TYPE CONTROL	YES	YES	YES	2

(*) Single letter code for amino acid changes at position 196 or 477 (as noted) in which wild type aspartate (D) is exchanged with an asparagine (N), glutamate (E), or lysine (K). "W/O" weak (<8% of wild-type) or no activity.

[000163] The mutant enzymes are useful for adding on a single GlcNAc or a single GlcUA onto the appropriate acceptor oligosaccharide. It appears that pmHAS$^{1-703}$ has two domains or two modules for transferring each sugar. One of ordinary skill in the art, given this specification, would be able to shift or to combine various domains to create new polysaccharide synthases capable of producing new polysaccharides with altered structures. Within such use, a variety of grafting techniques arise which utilize pmHAS$^{1-703}$ as the prototype. A graphical representation of each mutant as it relates to the pmHAS$^{1-703}$ sequence, is shown in FIG. 7.

[000164] The critical structural elements of the HA oligosaccharide acceptor or primer molecule are currently being tested and identified. The smallest acceptor molecule with activity tested thus far is an HA disaccharide, although it is anticipated that molecules as short as a monosaccharides will be suitable for use with the present invention.

[000165] Chemically synthesized oligosaccharides (ref. Halkes, K.M. et al., 1998, Carbohydrate Research, 309, p. 161-174) were tested to see if they could be elongated by pmHAS$^{1-703}$. Each sugar was added individually to a final concentration of 0.05 mM to a series of 50 µL reaction mixtures containing 50 mM Tris, pH 7.2, 1 M ethylene glycol, 0.1 M ammonium sulfate, 10 mM $MnCl_2$, 800 µM UDP-GlcNAc, 600 µM UDP-[^{14}C]GlcUA ($6x10^4$ dpm), and 2.5 µg pf pmHAS$^{1-703}$. After 20 minutes at 30°C, the HA polymer produced was quantitated by paper chromatography (polymer at the origin of the paper strip) and liquid scintillation counting (Jing and DeAngelis, 2000, Glycobiology, 10, p. 883-889).

Table VII

Sugar*	[^{14}C]GlcUA incorporation (*dpm*)
0	18
N-MP	16
AN-MP	24
NA-MP	140
ANA-MP	3540
NAN-MP	250
ANAN-MP	4000
NANA-MP	1710
NANAN-MP	2620
ANANAN-MP	3720

*Note: The sugar composition symbols: MP, methoxyphenyl group at the reducing end; N, GlcNAc; A, GlcUA.

[000166] It is obvious that the trisaccharide ANA (GlcUA-GlcNAc-GlcUA) is sufficient for high efficiency elongation by pmHAS, but certain disaccharides such as NA (GlcNAc-GlcUA), are also functional acceptors albeit at a lower efficiency than the longer sugars. Of course, one skilled in that art would expect that other sugar acceptors would be possible in light of the fact that pmHAS will elongate hyaluronic acid or chondroitin or chondroitin sulfate or heparin polysaccharides. The identity of the hexosamine and the availability of the hydroxyls (e.g. sulfated) may also be altered.

[000167] Recent data suggests that the pmHAS$^{1-703}$ enzyme has some flexibility with respect to the identity of the hexosamine group; i.e. other isomers will substitute for the GlcNAc sugar. For example, chondroitin pentamer [GalNAc-GlcUA-GalNAc-GlcUA-GalNAc], serves as an effective acceptor for pmHAS$^{1-703}$. Therefore, a synthetic molecule consisting of several hydroxyl groups, a pair of negatively charged groups (corresponding to the carboxyl groups of GlcUA sugar), and hydrophobic patches (analog of the carbon-rich side of the sugar ring) will work as a functional primer for pmHAS. Such an approach is not unprecedented as the polymerization of heparin, a glycosaminoglycan, can be primed with a rather simple aromatic xyloside instead of a complex proteoglycan core in vertebrate cells.

[000168] Computer modeling of HA oligosaccharides can visualize potential molecular shape. However, some proteins distort the sugar chains upon binding, thus making computer modeling somewhat more complicated. The most efficacious method of finding an artificial

primer is a combinatorial chemistry approach. Closely related series of molecules are screened by high-throughput assay methodologies in order to detect HA elongation. $pmHAS^{1-703}$ is then tested for the ability to add an HA polymer onto synthetic primer candidates in a typical 96-well plate format. For example, a series of synthetic peptides (1 to 8 residues) terminating with a GlcNAc group using conventional F_{moc} chemistry can be generated. Such peptides are particularly promising because they can adopt a variety of conformations and fit within the $pmHAS^{1-703}$ HA-binding pocket via an induced fit mechanism. Synthetic peptide chemistry is also much less cumbersome than carbohydrate chemistry. One of ordinary skill in the art, given the present specification, would be capable of using the known synthetic peptide chemistry techniques.

[000169] The amino acids are chosen with the goal of mimicking the properties of the GlcNAcGlcUA sugar repeats of HA. For example, glutamate or asparatate may be used as a substitute for the acid group of GlcUA, or glutamine or asparagine may be used as a substitute for the amide group of GlcNAc. Serine, threonine, or tyrosine can be used as substitutes for the hydroxyl groups and sugar rings in general. The peptide library terminates with a GlcNAc or GlcUA sugar group so that the demands on the $pmHAS^{1-703}$ enzyme's binding site and catalytic center are not overly burdensome. A vast variety of distinct peptides are made in parallel with a combinatorial approach; for example, with a hypothetical 6-7 residue peptide containing 1 to 3 different amino acids at each position, there are hundreds of possible peptides. The peptide combinatorial libraries will either be immobilized on plastic pins or plates.

[000170] The present invention also encompasses the development of a mutant version of pmHAS that utilizes a simpler molecule than an HA oligosaccharide as a primer. Chitopentaose (β1,4-GlcNAc homopolymer) is one such variant primer. Native pmHAS does not utilize chitopentaose as a primer, but a mutant pmHAS may elongate chitopentaose, a more readily available substance. The chitopentaose primer is attached to the solid phase by reductive amination to an amino-containing plate or to a carrier protein (albumin) for immobilization on a normal plastic plate. Various mutants could then be screened for function. Other potential non-sugar mimics contemplated for use are short poly(ethleneglycol)-based copolymers containing styrene, sulfonate, acrylate, and/or benzoate groups.

[000171] Certain experiments are useful for detecting a protein's binding sites. Photoaffinity labeling is used to cross-link a radioactive HA oligosaccharide analog containing an aryl azide to the $pmHAS^{1-703}$ protein. The binding site of the $pmHAS^{1-703}$ protein is obtained through peptide mapping and Edman sequencing. With this information, mutants are prepared with alterations at the binding site. In the chitopentaose example, removal of some of the basic residues of the HA-binding site (which normally contact the carboxylate of GlcUA) and

substitution of neutral polar residues would be chosen. As described above, a variety of site-directed mutants using a mutagenic oligonucleotide with mixed bases at certain positions have been generated. Such a mixed-base approach economizes on the number of custom oligonucleotides and transformations required. A high-throughput screen is then used to assess the ability of the mutant pmHAS to elongate the synthetic primer with a HA chain. An empirical approach can also be used to randomly mutate pmHAS$^{1-703}$ (either chemical mutagens or with a passage through a mutator strain) and then screen.

[000172] Recent work with the *E. coli* K5 KfiA and KfiC enzyme complex, which together polymerizes heparosan, differ from the hereinafter described pmHS1 and PmHS2, which are both single proteins that can transfer both sugars to the nonreducing end of acceptor molecules *in vitro*. In 2002, an *E. coli* K4 enzyme, called KfoC which is 60% identical to pmCS and that hybridizes to *pmCS*, SEQ ID NO:3, under standard stringency hybridizations conditions, was described as being a chondroitin polymerase that adds on chains to chondroitin acceptors. In particular, the present applicants used the *pmCS* gene DNA as a hybridization probe for detecting other chondroitin synthase genes and in particular, the *E. coli* K4 *kfoC* gene DNA. In general, a commercial Southern blot kit (Dig Hi-Prime, Roche) was used to label restriction fragments containing *pmCS* with digoxigenin probe. This probe was used to analyze a Southern blot (FIG. 8) containing a *Pst*I/*Eco*RI digest of Type F *Pasteurella multocida* genomic DNA (a positive control; **P lane**), a PCR product of the *kfoC* gene (corresponding to product of Ninomiya et al, 2002; **lane K**), or *Lambda Hin*dIII standard (**lane L**). The hybridization was carried out at 37 °C overnight in the manufacturer's buffer (Dig Easy Hyb) at 37 °C overnight. The blot was washed with 2X SSC, 0.1% SDS at 30 °C for 15 min twice, then for 30 min in 0.5X SSC, 0.1% SDS at 30 °C before using the manufacturer's Dig-antibody protocol for colorimetric detection. The *kfoC* band is apparent (**KfoC black arrow**) as well as the native *Pasteurella* gene (**white arrow**). No spurious hybridization signals were seen from other irrelevant DNA species. Therefore, the knowledge of the pmCS sequence can be used to identify other chondroitin synthase candidates by known standard methodology.

[000173] In order, to identify the important domains of the 972-residue pmHAS polypeptide, the protein was truncated at the amino- and/or the carboxyl- termini. Polymerase chain reaction with primers corresponding to various internal sequences was used to generate a series of recombinant proteins for expression (Table VIII).

Table VIII

Protein*	Localization	Enzyme Activity			SEQ ID NO:
		HAS	GlcNAc -Tase	GLCUA -Tase	
1-972	Membrane	+	+	+	2
437-972	Inclusion body	-	-	-	13
437-756	Inclusion body	-	-	-	14
1-756	Membrane	+	+	+	20
1-703	Soluble	+	+	+	9
1-650	Soluble	-	+	-	10
1-567	Inclusion body	-	-	-	21
152-756	Inclusion body	-	-	-	15

+, active; -, inactive

The different truncated proteins are described by their constituent amino acid residues.

[000174] The truncated polypeptides were expressed well in *E. coli* and the experimentally determined molecular weight corresponded to the predicted size (Fig. 9). In vitro assays were utilized to assess the HA synthase activity, or the two half-reactions, either GlcNAc-Tase or GlcUA-Tase, that comprise HA polymerization (Table VIII). Some of the truncations were inactive. $pmHAS^{1-756}$ (SEQ ID NO: 20), which lacks the carboxyl-terminal 216 amino acid residues, was an active HA synthase and, for the most part, membrane-associated. An interesting observation was that $pmHAS^{1-703}$ (SEQ ID NO: 9), which lacks a larger portion of the carboxyl terminus, retained HAS activity but was transformed into a cytoplasmic protein accounting for up to ~ 10% of the total cellular protein. Thus the carboxyl-terminus, especially residues 703-756, is responsible for the association of native pmHAS with the membrane. With the further deletion from carboxyl-terminus, $pmHAS^{1-650}$(SEQ ID NO: 10) was still expressed at a high level as a soluble protein, yet was inactive as a HA synthase. However, $pmHAS^{1-650}$ was capable of transferring GlcNAc to the nonreducing terminal GlcUA of HA-derived oligosaccharides. As expected from the lack of HAS activity, $pmHAS^{1-650}$ did not transfer GlcUA to HA oligosaccharides, which terminated with a GlcNAc residue. Thus residues 650-703 are required, either directly or indirectly, for transferring GlcUA to the HA chain. $pmHAS^{1-567}$ (SEQ

ID NO: 21), with a further truncation at the carboxyl terminus, and pmHAS$^{152-756}$ (SEQ ID NO: 15) were insoluble, inactive proteins. These latter mutant proteins are likely to be misfolded inclusion bodies as they were not dissolved by a buffer containing the detergents NP-40, sodium deoxycholate and SDS unless boiled; in contrast, full-length pmHAS was readily solubilized by this buffer at room temperature.

[000175] Site-directed mutagenesis of pmHAS$^{1-703}$. Based on similarities in the amino acid sequence and predicted topology, two families of HASs have been proposed. The only member of Class II, pmHAS, possesses motifs similar to two out of the seven putative conserved motifs of Class I HASs; these motifs contain DGS and DxD sequences. The pmHAS sequence has a duplication of a ~100-residue long element in the regions from residue 161-267 and from residue 443-547 with these conserved motifs. These two elements of pmHAS that contain the conserved motif are named domain A1 and domain A2, respectively. This nomenclature is based on the similarity of these pmHAS domains to the "A" domain proposed for other glycosyltransferases that make β-linked carbohydrates. FIG. 10 shows the amino acid alignment of the two putative domains and their relative position in pmHAS$^{1-703}$. The above truncation results show that the GlcNAc-transferase activity can be separated from the HA synthase activity of pmHAS. Therefore, the domain A1 is responsible for the GlcNAc-transferase function of HA synthase while domain A2 is responsible for GlcUA-transferase activity. pmHAS$^{1-703}$, a short polypeptide with complete HAS activity, was subjected to site-directed mutagenesis in order to further refine the results. We mutated the conserved aspartate residues (residue 196 and 477; underlined, FIG. 10) of the two DGS motifs in the two domains were mutated.

[000176] Six different mutants were produced containing the following changes: domain A1 - D196E, D196N, D196K, and domain A2 - D477N, D477E, D477K. Upon sequence verification of the complete open reading frame, it was found that mutants with D196K, D196N, or D477N also had spontaneous mutation of D702I. As it was the penultimate residue of pmHAS$^{1-703}$, and as pmHAS$^{1-650}$ was a functional GlcNAc-Tase, this undesired mutation does not greatly affect the interpretation of the results of the desired point mutations (as the results below demonstrate, the mutants with substitutions at D196 or D477 sharing the same D702I mutation had different transferase activities supporting this conclusion). All of the mutant proteins were produced at similar levels. All of the mutants were either inactive or made long HA polymer with low efficiency as measured by the full HAS assay (Table IX).

Table IX

Mutants	Enzyme Specific Activity		
	HAS	GlcNAc-Tase	GlcUA-Tase
D477N	2	200%	2%
D477K	0.3	70%	2%
D477E	4	50%	4%
D196N	0.1	0%	74%
D196K	0.01	3%	100%
D196E	0.3	7%	60%

Specific activities of various $pmHAS^{1-703}$ mutants. Equivalent amounts of $pmHAS^{1-703}$ proteins (based on Western blot) were assayed. The specific activities (average of duplicate determinations) are indicated as the percentage of the wild-type sequence $pmHAS^{1-703}$ (set as 100%). The specific activities (picomoles of monosaccharide transfer/mg of protein/min) for wild-type enzyme in the three different assays were: HAS, 37; GlcNAc-Tase, 63; GlcUA-Tase, 76.

[000177] However, $pmHAS^{1-703}$ domain A1 mutants containing D196E, D196K or D196N maintained high levels of GlcUA-transferase activity. On the other hand, $pmHAS^{1-703}$ domain A2 mutants containing D477E, D477K or D477N had high levels of GlcNAc-transferase activity implying that the two aspartate residues were critical for HA synthase function. Thus, two distinct transferase domains exist in the pmHAS enzyme; domain A1 is the GlcNAc-transferase and domain A2 is the GlcUA-transferase.

[000178] K_M analysis of mutants. In order to detect potential interaction or cross-talk between the two putative domains of pmHAS, the apparent affinity of the wild-type and the $pmHAS^{1-703}$ mutants were compared for the UDP-GlcNAc or for the UDP-GlcUA substrates by measuring their Michaelis constants (K_M) for the functional transferase activity. Titration of the UDP-sugars in the half assays for the GlcUA and GlcNAc transferases were performed (Table X).

Table X

Enzyme	K_M for UDP-GlcNAc (mM)	K_M for UDP-GLcUA (mM)
wild type	160 +/- 60	140 +/- 40
D477N	+/- 45	ND*
D477K	+/- 40	ND
D477E	150 +/- 30	ND
D196N	ND	240 +/- 140
D196K	ND	115 +/- 45
D196E	ND	140 +/- 35

K_M values for UDP-sugar precursors of pmHAS$^{1-703}$ and mutant proteins. The results ± standard deviation are shown. The apparent affinities of the functional glycosyltransferase activities of the various enzymes are similar. The typical level of radiolabel incorporation at the saturating UDP-sugar concentration using 1 mg of total protein/assay point was 500-1000 dpm [^{14}C]GlcA or 200-800 dpm [^{3}H]GlcNAc for the UDP-GlcNAc or UDP-GlcUA K_M values, respectively.
ND, not done.

[000179] The results indicate that the K_M values of the domain A1 or A2 mutants were not very different from the wild-type sequence pmHAS$^{1-703}$. Thus, the functional disruption of one glycosyltransferase domain of pmHAS does not affect greatly the other domain.

[000180] Complementation of HAS activity with two mutant proteins *in vitro*. The domain A1 and the domain A2 mutants fulfill the complete function of a HAS even if present on separate polypeptide molecules if the mutants are mixed together in the same reaction. The standard HA synthesis assay was performed with extracts containing either the truncated wild-type sequence pmHAS$^{1-703}$ enzyme, or a GlcNAc-Tase mutant enzyme (D196N) alone, or a GlcUA-Tase mutant enzyme (D477K) alone, or a mixture of the two mutant enzymes. These two mutants were selected as they were the least active in the HA synthase assay (Table IX). Equivalent amounts of wild-type pmHAS$^{1-703}$ polypeptide (2 µg of total protein) or mutant pmHAS$^{1-703}$ polypeptide (based on Western blot analysis) were used for these assays. In the mixture, the same amount of each mutant polypeptide was added (equivalent to 4 µg of total protein of wild-type extract). The D196N mutant alone or the D477K mutant alone did not produce detectable amounts of HA chains (FIG. 11), but when the mutant polypeptides were incubated together, along with a HA oligosaccharide acceptor (4-10 sugars long), longer HA polymers were made. The amount and the rate of HAS activity of the combination of the two mutants was similar to the parallel reaction containing the wild-type pmHAS$^{1-703}$. Without HA oligosaccharide acceptor, the wild-type pmHAS$^{1-703}$ enzyme could still make HA, albeit with lower efficiency (2 µg total protein in 3 hr assay incorporated 220 dpm). The combination of the two mutant extracts, however, did not make detectable amounts of HA polymer in absence of

the HA acceptor (incorporation ≤4 dpm). These results suggest that in the presence of HA oligosaccharide acceptor, the two kinds of transferases could work together and sequentially transfer GlcNAc and GlcUA monosaccharides to an existing HA chain in an alternating fashion. Apparently chain initiation requires two active transferases to be present on the same polypeptide.

***P. multocida* Chondroitin Synthase pmCS**

[000181] As mentioned previously, chondroitin $[\beta(1,4)GlcUA\text{-}\beta(1,3)GalNAc]_n$, heparin/heparan $[\alpha(1,4)GlcUA\text{-}\beta(1,4)GlcNAc]_n$, and hyaluronan $[\beta(1,4)GlcUA\text{-}\beta(1,3)GlcNAc]_n$ are the three most prevalent GAGs found in humans. In the former two polymers, usually n=20 to 100 while in the case of HA, $n=10^{3-4}$. Chondroitin and heparin/heparan, but not HA, are synthesized as glycoproteins and are sulfated at various positions in vertebrates. A substantial fraction of the GlcUA residues of heparin are epimerized to form iduronic acid. Many lower animals possess these same GAGs or very similar molecules. A chondroitin synthase from *P. multocida* (pmCS) is described and enabled in copending U.S. Serial No. 09/842,484 which is expressly incorporated herein in its entirety by reference.

[000182] Briefly, the glycosyltransferase responsible for polymerizing the chondroitin backbone component of the capsular polysaccharide has also been molecularly cloned and was named pmCS (SEQ ID NO:4). The pmCS enzyme appears to be a close homolog of the pmHAS enzyme (FIG. 12). In pmHAS one domain, called A1, is responsible for GlcNAc transfer and the other domain, called A2, is responsible for GlcUA transfer. Comparison of the pmHAS and the pmCS sequences reveals that the majority of the sequence differences exist in the A1 domain. The pmCS enzyme transfers a different hexosamine, GalNAc, thus this observation is consistent with the two-domain structure for pmHAS.

[000183] Mutant enzymes derived from the soluble $pmCS^{1-704}$ parental dual-action chondroitin synthase were also created with the ability to elongate HA or chondroitin-based oligosaccharides by adding a single β3-GalNAc monosaccharide to the non-reducing terminus. The mutants were formed by targeting the DXD motif in Domain A2 (also found in pmHAS) by site-directed mutagenesis (same general procedure as with pmHAS); the two aspartate (D) groups were converted into asparagine (N) residues forming the "NXN" mutants. Several independent clones producing mutant $pmCS^{1-704}$ NXN enzyme were assayed individually for the ability to transfer [^{3}H]GalNAc to HA oligosaccharides using UDP-GalNAc in analogy to pmHAS transferring [^{3}H]GalNAc to HA oligosaccharides using UDP-GlcNAc as described hereinabove. The NXN mutants could transfer a single GalNAc sugar like the wild-type sequence $pmCS^{1-704}$ enzyme.

[000184] The NXN mutants could not, however, make long chondroitin chains when

assayed in a different system that only detected the addition of both GlcUA and GalNAc. This system utilizes leech hayluronidase-generated HA8-12mer oligosaccharide (this acceptor has a non-reducing end GlcNAc; 1.5 ug), 15 mM UDP-GlcUA, 0.1 mM UDP-[^{3}H]GalNAc ($4.4x10^5$ dpm) in 20 µL reaction mixtures containing 50 mM Tris, pH 7.2, 1 M ethylene glycol, 0.1 M ammonium sulfate, 10 mM $MnCl_2$. Extracts containing either the wild-type $pmCS^{1-704}$ (CS-WT) or the NXN mutant extracts were assayed for 120 minutes at 30°C. After the reaction, the labeled polymer produced was quantitated by paper chromatography (polymer at the origin of the paper strip) and liquid scintillation counting. The NXN mutants (3 different clones: 2, 3, or 7) do not display high incorporation in this assay because these single-action enzymes cannot add the required GlcUA to the acceptor terminus: without prior GlcUA transfer, the radioactive GalNAc is never added (See Table XI). In contrast, the parental dual-action pmCS enzyme can perform GlcUA addition thus allowing the radioactive GalNAc to be added; furthermore, multiple rounds of GlcUA and GalNAc addition are possible with wild-type enzyme yielding a very high signal. Overall, such controllable single-action enzymes are useful for bioreactor systems for oligosaccharide syntheses or for construction of sugar libraries.

Table XI

Enzyme	[^{3}H]GalNAc (dpm)
None	2
CS-NXN-2	141
CS-NXN-3	152
CS-NXN-7	242
CS-WT	173,000

Additional pmHAS Mutants

[000185] pmHAS and pmCS both utilize two relatively independent glycosyltransferase sites. Other sequence motifs are also discussed with respect to their roles in polysaccharide biosynthesis. Hereinafter is the analysis of truncated pmHAS proteins used to delineate essential regions.

[000186] In order to analyze the contribution of the amino terminal region of pmHAS, various recombinant truncated polypeptides ($pmHAS^{46-703}$ SEQ ID NO:27, $pmHAS^{72-703}$ SEQ ID NO:28, $pmHAS^{96-703}$ SEQ ID NO: 29 and $pmHAS^{118-703}$ SEQ ID NO:30) were produced in *E. coli*. The experimentally determined molecular weights corresponded to the predicted sizes. The truncated versions $pmHAS^{46-703}$ and $pmHAS^{72-703}$ were as active as $pmHAS^{1-703}$, a soluble

polypeptide with complete HAS activity. pmHAS$^{96-703}$ expressed at a very low level compared with other constructs but was active. pmHAS$^{118-703}$ expressed better than pmHAS$^{96-703}$ and still elongated HA chains. Therefore, further deletion beyond residue 72 appears to affect the overall folding efficiency of the entire polypeptide. Observation of lower molecular weight degradation bands derived from pmHAS$^{118-703}$ on Western blots also suggests that improper folding occurs to some extent. Overall, these findings suggest that the amino-terminal 117 residues are not required for HA synthase activity.

[000187] It was discussed hereinabove that pmHAS$^{1-650}$ (SEQ ID NO:10) lost its GlcUA-transferase activity. To further delineate the GlcUA-transferase domain within the carboxyl terminal region, two slightly longer mutants, pmHAS$^{1-668}$ SEQ ID NO: 31 and pmHAS$^{1-686}$ SEQ ID NO: 32 were created. Both mutants also could not polymerize HA due to the loss of GlcUA-transferase activity, indicating that the carboxyl-terminal boundary of the GlcUA-transferase resides between residues 686 and 703.

[000188] Others of ordinary skill in the art have used hydrophobic cluster analysis to identify two types of domains conserved in a variety of β-linked glycosyltransferases that use nucleotide diphospho sugar as donors, termed Domain A and Domain B. Characterization of two conserved DGS motifs in the two A domains of pmHAS indicate that the two aspartate residues are essential for HAS activity. The existence of a third potential DGS sequence motif in pmHAS is also located at position 563-565. In order to determine if this motif is critical for synthase activity in the same manner as the other two DGS motifs, D563 of pmHAS$^{1-703}$ was mutated into a glutamate, asparagine or lysine residue. All of the mutants behaved like wild-type pmHAS$^{1-703}$ indicating that the third motif DGS is not essential for the catalytic activity of pmHAS. This also demonstrates that certain residues may be changed, but the enzyme remains a functional synthase – i.e. with respet to the "functionality" language of the hereafter appended claims.

[000189] The DXD motif is found in many glycosyltransferases. pmHAS has two DXD motifs, one in domain A1 and another in domain A2 (FIG. 13). X-ray crystallography of the *Bacillus* SpsA protein/UDP-complex suggests that the DXD motif is involved in binding metal ion coordinated with the beta phosphate and the ribose moiety of the UDP-sugar. The involvement of the individual aspartate residues of DXD in pmHAS, therefore, was characterized. The aspartate residues (residue 247, 249, 527 or 529) of the two DXD motifs of pmHAS$^{1-703}$ were mutated in the two domains. Mutants were produced containing the following changes in domain A1 - D247E (SEQ ID NO:33), D247N (SEQ ID NO:34), D247K (SEQ ID NO:35), D249E (SEQ ID NO:36), D249N (SEQ ID NO:37), or D249K (SEQ ID NO:38) and in domain A2 - D527N (SEQ ID NO:39), D527E (SEQ ID NO:40), D527K (SEQ ID NO:41), D529E (SEQ ID NO:42), D529N (SEQ ID NO:43), or D529K (SEQ ID NO:44). Upon sequence

verification of the complete open reading frame, mutants with D247N, D249K, D529E and D527K were found to also have a mutation of D702I that did not affect HAS activity. All of the mutant proteins were produced at similar levels in soluble form. *In vitro* assays were utilized to assess the HA synthase activity (e.g. polymerization of long HA chains), or the two half-reactions, either GlcNAc-transferase or GlcUA-transferase activity. All of the mutants were inactive as HA synthases except D529E which had only 10% of the wild type activity (Table XII).

[000190] As predicted, the enzymes containing mutations at position 247 or 249 (domain A1 mutants) maintained high levels of GlcUA-transferase activity. On the other hand, the enzymes containing mutations at position 527 or 529 (domain A2 mutants) had high levels of GlcNAc-transferase activity. Therefore, all of the four aspartate residues were critical for HA synthase function. These results confirm the model of two distinct transferase sites in a single pmHAS polypeptide; domain A1 is essential for GlcNAc-transferase activity and domain A2 is essential for GlcUA-transferase activity.

Table XII

Enzyme	**Specific Activity**		
	HAS	GlcNAc-Transferase	GlcUA-Transferase
D247N	<0.1	<0.1%	110%
D247K	<0.1	<0.1%	130%
D247E	<0.1	<0.1%	90%
D249K	<0.1	<0.1%	100%
D249E	<0.1	<0.1%	105%
D527K	<0.1	115%	<0.1%
D527E	<0.1	120%	0.1%
D529N	<0.1	230%	<0.1%
D529K	5%	360%	<0.1%
D529E	10%	110%	15%

Specific activities of the various pmHAS$^{1-703}$ DXD mutants. Equivalent amounts of pmHAS$^{1-703}$ proteins (based on Western blot) were assayed. The specific activities are indicated as the percentage of the wild-type sequence pmHAS$^{1-703}$ (set as 100%). The specific activities for wild-type enzyme in the three assays were 6-34 picomole of monosaccharide transfer /mg/min. The DXD motif of each domain is involved in HA polymerization.

[000191] The two DXD motifs of pmHAS are predicted to be involved in metal ion binding based on the SpsA structure. Experiments were designed to examine (a) if other metal ions

could rescue mutant activity and (b) if the two separate active sites have similar metal ion preference. The presence of Co^{2+}, Mg^{2+} or Ca^{2+} did not convert the DXD mutants into functional HASs. GlcNAc-transferase or GlcUA-transferase assays were performed with wild-type pmHAS$^{1-703}$ in the presence of 20 mM Mn^{2+}, Co^{2+} or Mg^{2+}. Although the highest activities were obtained in the presence of 20 mM of Mn^{2+}, the GlcNAc-transferase activity preferred Co^{2+} over Mg^{2+} while the GlcUA-transferase activity preferred Mg^{2+} over Co^{2+} (Table XIII).

Table XIII

Enzyme	Specific Activity			
	GlcNAc-Transferase		GlcUA-Transferase	
	Co^{2+}	Mg^{2+}	Co^{2+}	Mg^{2+}
D247N			15%	52%
D247K			1%	37%
D247E			9%	55%
D249N			14%	58%
D249K			10%	46%
D527E	87%	27%		
D529N	75%	59%		
Wt	77%	39%	18%	66%

Metal ion preference of the GlcNAc-transferases and the GlcA-transferase activities. Equivalent amounts of wild type pmHAS$^{1-703}$ protein (wt) or DXD mutants were assayed in the presence of 20 mM of Mn^{2+}, Co^{2+} or Mg^{2+}. The activities are indicated as the percentage of their activities in the presence of Mn^{2+} (set as 100%). Overall, Mn^{2+} is the best cofactor, but in its absence, the GlcNAc-transferase preferred Co^{2+} while the GlcUA-transferase preferred Mg^{2+}. The active sites of domain A1 and A2 are similar yet distinct.

[000192] Similar results were obtained when assays were performed with the pmHAS$^{1-703}$ mutants that have only a single transferase activity. In a preferred embodiment, both Ds (aspartates) are mutated to Ns (asparagines): one D can be changed to N but the resulting mutant enzyme may retain some "sloppiness" - i.e. the enzyme may incorporate both natural sugars. As such, it may be preferred to mutate both Ds of the DXD motif to Ns in order to truly "kill" or knock-out the enzymatic activity of the domain.

[000193] In the pmHAS polypeptide sequence, there is a segment similar to portions of mammalian UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferases (ppGaNTransferases) that catalyzes the initial step for making the oligosaccharide moiety on O-linked glycoproteins. The W366GGED370 motif, which resides between the putative domain A1 and domain A2, does not exist in the sequences of other HA synthases from *Streptococcus*,

separate transferase sites with respect to pmCS, but the amino-terminal half is a GalNAc-transferase while the carboxyl-terminal half is a GlcUA-transferase. Thus, swapping the carboxyl-terminal GlcUA-transferase site between pmHAS and pmCS does not affect the sugar polymerizing activity. On the other hand, swapping of the amino-half of either pmHAS or pmCS changes the hexosamine transfer specificity. In order to test such "swapping" abilities, domain swapping between pmHAS and pmCS was performed by the PCR-overlapping-extension method (as described in Horton et al., 1989, which is expressly incorporated herein by reference in its entirety).The active truncated versions of the synthases, $pmCS^{1-704}$ and $pmHAS^{1-703}$, were used as the starting materials for the construction. Residues 427/428 of pmHAS and the equivalent site of pmCS, residues 420/421, were chosen as the initial splicing site based on comparisons of the amino acid sequences of pmHAS, pmCS and other GlcNAc-transferases.

[000196] The combination of residues 1-427 from pmHAS and residues 421-704 from pmCS (pmAC construct: SEQ ID NO:51) resulted in an active HAS. The opposite combination, consisting of residues 1-420 from pmCS and residues 428-703 from pmHAS (pmBD construct: SEQ ID NO:52), resulted in an active chondroitin synthase (Table XV).

Table XV

Enzyme	Chondroitin Synthase	HA synthase
$pmHAS^{1-703}$	-	+
$pmCS^{1-704}$	+	-
pm-AC	-	+
pm-BD	+	-

Activity of chimeric or hybrid *Pasteurella* synthases. The wild type enzymes and the chimeric or hybrid constructs (**pm-AC**, $pmHAS^{1-427}$-$pmCS^{421-704}$; **pm-BD**, $pmCS^{1-420}$-$pmHAS^{428-703}$) were tested in the HA or the chondroitin synthase assays. Domain A1 is responsible for hexosamine transfer and domain A2 is responsible for GlcUA transfer.

[000197] This finding indicates that the domain A1 dictates hexosamine transfer specificity. Also, the source of the GlcUA-transferase domain A2 does not affect the specificity of either the GalNAc-transferase or the GlcNAc-transferase activity. The two single-action transferase sites of pmHAS and pmCS are relatively independent.

[000198] The DXD motif is conserved in many glycosyltransferases from different families and the aspartates have been shown to be crucial for activity in enzymes whose function and sequences are highly divergent. pmHAS possesses a DXD motif in both domain A1 and domain

vertebrates, or *Chlorella* virus. To study the function of the WGGED motif in pmHAS, E369 or D370 were mutated. Six different mutants were produced each containing one of the following changes, E369D (SEQ ID NO:45), E369Q (SEQ ID NO:46), E369H (SEQ ID NO:47), D370E (SEQ ID NO:48), D370N (SEQ ID NO:49), or D370K (SEQ ID NO:50). All the mutants were expressed at comparable levels with the wild type enzyme. Based on the results of the HAS assays and the two half assays, mutation at either of these two sites resulted in the loss of only GlcNAc-transferase activity, but not the GlcUA-transferase activity (Table XIV), suggesting that the WGGED motif in pmHAS-D is essential for GlcNAc-transferase activity.

Table XIV

Enzyme	Specific Activity		
	HAS	GlcNAc-Transferase	GlcUA-Transferase
D370N	<0.1	1%	80%
D370K	<0.1	2%	80%
D370E	1%	<0.1%	105%
E369H	<0.1	5%	130%
E369D	<0.1	1%	55%
E369Q	1%	1%	60%

Specific activities of the $pmHAS^{1-703}$ WGGED mutants. Equivalent amounts of $pmHAS^{1-703}$ proteins (based on Western blot) were assayed. The activities are indicated as the percentage of the wild type $pmHAS^{1-703}$ (100%). The WGGED motif is involved in the transfer of GlcNAc.

[000194] As described hereinabove, a combination of two DGS motif mutants, D196N, a GlcUA-transferase and D477K, a GlcNAc-transferase, fulfill the complete function of a HAS when mixed together in the same reaction along with a HA oligosaccharide acceptor. Hereinafter the standard HA synthesis activity assay was performed with several different combinations of DXD or WGGED mutants. One GlcNAc-transferase mutant enzyme (a D527 or D529 mutant) and one GlcUA-transferase mutant enzyme (a D247, D249, E370, or D369 mutant) were combined in these tests. When the mutant polypeptides were incubated together, along with a HA oligosaccharide acceptor (4-10 sugars long), HA polymers were made. This demonstration further enables the proposition that two independent transferase sites sequentially transfer GlcNAc and GlcUA monosaccharides to an existing HA chain in an alternating fashion.

[000195] The chondroitin synthase, pCS, from Type F P. multocida is about 90% identical to pmHAS at the protein level. The majority of sequence differences exist in the vicinity of the domain A1 of pmHAS while their carboxyl-terminal halves are almost identical (described hereinabove). This is to be expected because the carboxyl-terminal half of pmHAS contains domain A2 which has the GlcUA-transferase active site. The pmCS also possesses two

A2. Mutagenesis of any of these four aspartates indicates that they are involved in HA polymerization in agreement with the presumed critical role of the motif. Mutation of the domain A1 DXD results in the loss of only GlcNAc-transferase activity while mutation of the domain A2 DXD results in the loss of only GlcUA-transferase activity.

[000199] Although the importance of the DXD motif was previously hypothesized, its function was not clear until very recently. Based on an X-ray crystal structure of SpsA, a family 2 glycosyltransferase, the DXD motif is now known as a nucleotide-binding element. The first aspartate forms a hydrogen bond with the ribose ring and the second aspartate coordinates with the metal cation bound to the phosphate to assist leaving group departure. The involvement of the DXD motif in nucleotide binding and in metal ion interaction is supported by several other available glycosyltransferase structures which were solved later, including bovine β4-galactosytransferase, rabbit N-acetylglucosaminyltransferase I (in which the motif is in the form of EDD and the last aspartate, D213, makes the only direct interaction with the bound Mn^{2+}), and human β1,3-glucuronyltansferase I. A retaining enzyme, bovine β1,3-galactosyltransferase, contains a DXD motif with a similar structure for UDP-binding.

[000200] In the case of pmHAS, which possesses two separate transferase sites each with a DXD motif, each transferase site contains a set of UDP-precursor-binding sites and catalytic residues. The two DXD motifs of each site are similar but not identical. The two half-activities of pmHAS prefer Mn^{2+}, but the two sites differ in their relative preference for Co^{2+} and Mg^{2+}. The underlying reason for this selectivity is not known, but it can be speculated that various metal ions confer different coordination angles and geometry to the sugar nucleotide/enzyme binding site complex. Indeed, the X-ray crystal structure of SpsA showed that the two phosphate groups of UDP are ordered differently in the presence of Mn^{2+} or Mg^{2+}.

[000201] The WGGED motif was first noted among β4-galactosyltransferases and a similar motif, WGXEXXE, was found among UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferases. Residues in this Gal/GalNAcT motif have been shown to be essential for enzyme activity. The X-ray crystal structure of bovine β4-galactosyltransferase showed that E317D residues in WGGE317D segment are located at the bottom of the proposed UDP-Gal binding pocket. It was speculated that the E or the D residue was a good candidate for making the nucleophilic attack on the 4-hydroxyl group of the acceptor substrate GlcNAc ring. The assignment of the role of catalytic base to an E or D residue is supported by structural studies on several other glycosyltransferases. There is only one WGGED motif in pmHAS. The GlcNAc-transferase, but not the GlcUA-transferase, activity of pmHAS depends on the WGGED motif. The homologous pmCS enzyme, also possesses this motif. The WGGED motif plays the same role in the hexosamine transfer reaction of the *Pasteurella* synthases as

it does in the Gal-/GalNAc-transferases.

[000202] Saxena proposed two types of putative domains, Domain A and Domain B, among many beta-glycosyltransferases that use nucleotide diphospho sugars as donors. Saxena noticed that processive enzymes, which add a number of sugar residues without releasing the nascent chain, possess both Domains A and B, while those enzymes that add a single sugar residue have only Domain A. In general, Domain A resides in the N-terminal half of the polypeptide and possesses two invariant Asp residues, while Domain B resides in the C-terminal half and with an invariant Asp residue along with a characteristic QXXRW motif. Saxena, et al. hypothesized that the production of heteropolysaccharides with alternating sugar residues, such as HA, is fulfilled by specializing Domain A for one sugar and Domain B for a different sugar.

[000203] The only known member of Class II HA synthases, pmHAS, possesses two tandem copies of Domain A and does not contain Domain B. Data from the activity analysis of the truncated versions and the point mutants of pmHAS indicate that two active sites coexist in one polypeptide. Overall, pmHAS appears to be a polypeptide with two coordinated but intrinsically nonprocessive activities. Support for this characterization is found in the pmHAS mutant *in vitro* complementation study; two distinct polypeptide molecules can act together to polymerize HA chains in a rapid fashion. The HA chain must be released by one mutant to be acted on by the other mutant. The distinct Class I HA synthases, however, do not appear to release the nascent chain during synthesis.

[000204] PmCS is 90% identical to pmHAS and possesses two similar sets of putative nucleotide-binding elements. Therefore, pmCS utilizes the same structural organization and general catalytic mechanism as pmHAS. Dissection of the two transferase activities in pmHAS provides direct evidence for a two-active center model (FIG. 13). The *E. coli* K4 chondroitin polymerase (named a "polymerase" rather than "synthase" due to its apparent absolute requirement for an acceptor chain), KfoC, was recently reported (Ninomiya, et al., 2002). This protein is about 60% identical to pmHAS and pmCS, and thus probably utilizes similar motifs and domains. Another case of the "one polypeptide, two active center" model is the eukaryotic glycosyltransferase FT85, an enzyme involved in the glycosylation of Skp1 protein in Dictyostelium. This bifunctional glycosyltransferase mediates the ordered addition of β1,3-linked Gal and α1,2-linked Fuc to the Skp1 glycomoiety. The overall architecture of FT85 resembles pmHAS in that it contains two glycosyltransferase domains.

[000205] In the live bacterium, the pmHAS or the pmCS polypeptide engages with the polysaccharide export apparatus. In order to retain the nascent chain during polymerization *in vivo*, other proteins may help maintain the interaction of the transferase with the elongating

GAG chain. The catalytic reaction mechanism and/or the intrinsic nature of pmHAS or pmCS are probably not the major chain retaining mechanisms.

pmHS1 and PmHS2 Identification and Molecular Cloning.

[000206] As stated hereinabove, *Pasteurella multocida* Type D, a causative agent of atrophic rhinitis in swine and pasteurellosis in other domestic animals, produces an extracellular polysaccharide capsule that is a putative virulence factor. It has been reported that the capsule of Type D was removed by treating microbes with heparin lyase III. A 617-residue enzyme, pmHS1 (SEQ ID NOS: 5 and 70), and a 651-residue enzyme, PmHS2 (SEQ ID NO: 8), which are both authentic heparosan (unsulfated, unepimerized heparin) synthase enzymes have been molecularly cloned and are presently claimed and disclosed in copending U.S. Application Serial No. 10/142,143, incorporated herein previously by reference. Recombinant *Escherichia coli*-derived pmHS1 or PmHS2 catalyzes the polymerization of the monosaccharides from UDP-GlcNAc and UDP-GlcUA. Other structurally related sugar nucleotides do not substitute. Synthase activity was stimulated about 7- to 25-fold by the addition of an exogenous polymer acceptor. Molecules composed of ~500 to 3,000 sugar residues were produced *in vitro*. The polysaccharide was sensitive to the action of heparin lyase III but resistant to hyaluronan lyase. The sequence of pmHS1 enzyme is not very similar to the vertebrate heparin/heparan sulfate glycosyltransferases, EXT1/2 (SEQ ID NOS: 65/66), or to other *Pasteurella* glycosaminoglycan synthases that produce hyaluronan or chondroitin. Certain motifs do exist however, between the pmHS1, pmHS2, and KfiA (SEQ ID NO:65) and KfiC (SEQ ID NO:64) thereby leading to deduced amino acid motifs that are conserved throughout this class of GAG synthases for the production of heparin/heparosan. The pmHS1 and PmHS2 enzymes are the first microbial dual-action glycosyltransferase to be described that form a polysaccharide composed of β4GlcUA-α4GlcNAc disaccharide repeats. In contrast, heparosan biosynthesis in *E. coli* K5 requires at least two separate polypeptides, KfiA and KfiC, to catalyze the same polymerization reaction.

[000207] *Molecular Cloning of the Type D P. multocida Heparosan Synthase* - A PCR product which contained a portion of the Type D UDP-glucose dehydrogenase gene was used as a hybridization probe to obtain the rest of the Type D *P. multocida* capsular locus from a lambda library. We found a functional heparosan synthase, which we named pmHS1, in several distinct Type D strains from different host organisms isolated around the world (i.e. A2 clone SEQ ID NOS:5 and 6; bioclone SEQ ID NOS:69 and 70). In every case, an open reading frame of 617 residues with very similar amino acid sequence (98-99% identical) was obtained. In the latter stages of our experiments, another group deposited a sequence from the capsular locus of a Type D organism in GenBank [15]. In their annotation, the carboxyl terminus of the pmHS1

homolog is truncated and mutated to form a 501-residue protein that was called DcbF (GenBank Accession Number AAK17905) (SEQ ID NOS:61 and 62). No functional role for the protein except "glycosyltransferase" was described and no activity experiments were performed. As described herein, membranes or cell lysates prepared from *E. coli* with the recombinant *dcbF* gene do not possess heparosan synthase activity. The gene annotated as *DcbF* (SEQ ID NO:62) is truncated at the carboxyl terminus in comparison to the presently claimed and described *P. multocida* HS clones. The truncated (T) or the full-length (FL) open reading frames of DcbF were cloned into the expression system pETBlue-1 vector, as described hereinabove. Membranes isolated from the same host strain, *E. coli* Tuner with the various recombinant plasmids were tested in HS assays with both radiolabeled UDP-sugars. The results of these experiments are summarized in Table XVI.

TABLE XVI

Clone	**[14C]GlcUA Incorp.**	**[3H]GlcNAc Incorp.**
	(dpm)	**(dpm)**
Negative Control	160	40
B1(FL)	710(*)	1040(*)
012(T)	40	265
013(T)	70	1610
019(T)	55	1105
N2(T)	70	1910
N4(T)	70	880
N5(T)	80	650

[000208] Five-fold less FL enzyme than T enzymes were tested in these parallel assays. At most, only a single GlcNAc sugar is added to the exogenously supplied acceptor in the truncated enzymes (T). Full-length HS from Type D *P. multocida*, however, adds both sugars (*) to the nascent chain. Thus, the previously annotated and deposited *DcbF* gene *is not* a

functional heparosan synthase.

[000209] Another deduced gene was recently uncovered by the University of Minnesota in their Type A *P. multocida* genome project, called *PmHS2* (GenBank Accession Number AAK02498), encoding 651 amino acids that are similar to pmHS1 (73% identical in the major overlapping region). However, the PmHS2 gene (SEQ ID NO:7) is not located in the putative capsule locus. This group made no annotation of the function of PmHS2. Our studies show that this PmHS2 protein (SEQ ID NO:8) also polymerizes GlcUA and GlcNAc residues to form heparosan. We also found that a Type D strain and a Type F strain also appear to contain a homologous *PmHS2* gene as shown by PCR and activity analysis.

[000210] As mentioned before, during the pmHS1 cloning project in the present Applicant(s)' laboratory, investigators at the Univ. of Minnesota published the complete genome of a *Pasteurella multocida* isolate. The fragments of the presently claimed and disclosed *pmHS1* gene were utilized as the query in a BLAST search against this *P. multocida* genome. A gene annotated as *pmHS2*, but with no ascribed, predicted or demonstrated function was found to be very similar to the *pmHS1* gene. The *pmHS2* gene is not in the main capsule locus found by either the DeAngelis or the Adler groups. The *pmHS2* open reading frame was obtained from two different encapsulated strains: Type A (P-1059 from a turkey - this strain is not the same as the Univ. of Minnesota strain - clones denoted as "A") and Type D (P-3881 from a cow - clones denoted as "D"). The *pmHS2* gene was amplified from chromosomal templates prepared by method of Pitcher *et al* (*Letters in Applied Microbiology*, 1989 which is expressly incorporated herein by reference in its entirety). PCR with *Taq* polymerase (18 cycles) using custom flanking oligonucleotide primers that correspond to the region of the start codon and the stop codon of *pmHS2*. An appropriate size amplicon corresponding to the *pmHS2* gene was found in both Type A and D strains; this result was rather unexpected if one considers that the capsular compositions are HA and N-acetylheparosan polysaccharides, for Type A and Type D strains, respectively. The resulting ~1.9 kilobase PCR amplicons were ligated into an expression vector, pETBlue-1 (Novagen), transformed into the cloning host, *E. coli* Novablue (Novagen), and selected on LB carbenicillin and tetracycline plates at 30°C. The colonies were screened for the presence of insert in the proper orientation by PCR with a combination of vector and insert primers. Clones were streak isolated, small cultures were grown, and preparations of the plasmid DNA were made. The plasmids were transformed into the expression host, *E. coli* Tuner (Novagen), and selected on LB with carbenicillin and chloramphenicol.

[000211] After streak isolation, small cultures were grown at 30°C as the starting inoculum (1:100) for larger cultures (50 ml) for protein expression and activity assay. These cultures

were grown in the same LB supplemented with 1% casein amino acids and trace element solution with vigorous shaking (250 rpm) at 30°C. The cells were grown to mid-logarithmic phase (2.5 hours), induced with 0.5 mm IPTG, and grown for 4.5 hours. Cells were collected by centrifugation and frozen at -80°C overnight. The membrane preparations were isolated by cold lysozyme/ultrasonication method of DeAngelis *et. al* (*J. Biol. Chem.*,1998; pmHAS isolation the contents of which are expressly incorporated herein in their entirety) except that 0.1 mM mercaptoethanol was used as the reducing agent. The membranes were assayed for radioactive sugar incorporation and descending paper chromatography (according to the methodology of DeAngelis and Padget-McCue, *J. Biol. Chem.*, 2000, the contents of which are expressly incorporated herein in their entirety).

[000212] In general, a mixture with membranes, 50 mM Tris, pH 7.2, 10mM $MgCl_2$, 10 mM $MnCl_2$, 0.4mM UDP-[^{3}H]GlcNAc, 0.2 mM UDP-[^{14}C]GlcUA, and heparin oligosaccharide acceptor (2 µg uronic acid) were incubated at 30ºC for 2.5 hours before analysis by paper chromatography. As expected for a polysaccharide synthase, both sugars were incorporated into polymer (Table XVII). Negative controls using membranes from a plasmid with an irrelevant control insert, did not show incorporation. Therefore, PmHS2 is a dual-action synthase capable of sugar biosynthesis as shown by functional expression of activity of one recombinant gene in a foreign host that normally does not make GlcUA/GlcNAc polymers. The relaxed specificity of UDP-sugar incorporation of PmHS2 should be of use for the design and production of new polymers with altered characteristics.

TABLE XVII

In vitro incorporation of sugar by membranes containing recombinant pmHS2.

CLONE	[^{3}H]GlcNAc (dpm)	[^{14}C]GlcUA (dpm)
PmHS2-A2	50,400	54,900
PmHS2-A4	39,100	41,000
PmHS2-D4	32,500	34,200
PmHS2-D7	44,800	46,600

[000213] The typical background for negative controls is less than 200 dpm incorporation. Type A and Type D isolates have the PmHS2, a synthase that incorporates both GlcUA and GlcNAc sugars. (A=Type A; D = Type D; # = independent clone number) .

[000214] Table XVIII shows PmHS2 Sugar Specificity test results. The experiments summarized in Table XVIII are similar to the experiments summarized in Table XVII (with less enzyme) *except* that other UDP-sugars that are not normally found in heparin or heparosan

were also tested (note - 60 minute incubation times, 50 µl reactions). The Type A and the Type D enzymes behave in a similar fashion with relaxed sugar specificity in this test. The PmHS2 system can add a glucose instead of a GlcNAc sugar. The ability to co-polymerize the sugars

TABLE XVIII

Panel I. Type A PmHS2-A2

2nd Sugar	[3H]GlcNAc Incorporated into Polymer (dpm)
none	450
UDP-GlcUA	12,900
UDP-GalUA	400
UDP-Glc	430

2nd Sugar	[14C]GlcUA Incorporated into Polymer (dpm)
none	60
UDP-GlcNAc	7,700
UDP-GalNAc	60
UDP-Glc	985

Panel II. Type D PmHS2-D7

2nd Sugar	[3H]GlcNAc Incorporated into Polymer (dpm)
None	570
UDP-GlcUA	13,500
UDP-GalUA	530
UDP-Glc	500

2nd Sugar	[14C]GlcUA Incorporated into Polymer (dpm)
None	60
UDP-GlcNAc	6,500
UDP-GalNAc	40
UDP-Glc	660

Table XIX. Acceptor Usage of PmHS2 from Types A and D

The Type A and the Type D clones were tested for stimulation by addition of the Type D polysaccharide acceptor (described hereinbefore with respect to pmHS1). Weaker stimulation of activity by acceptor on pmHS2 was observed in comparison to pmHS1 (comparison is not shown here).

[^{14}C-GlcUA] incorporation		
Clone	**Acceptor**	**NO Acceptor**
A2	1560	1210
D7	1240	1080

that compose the authentic heparin backbone were tested by performing two parallel reactions:

UDP-[^{14}C]GlcUA + various combinations of 2nd UDP-sugars.

UDP-[^{3}H]GlcNAc + various combinations of 2nd UDP-sugars.

[000215] *P. multocida* Type F-derived recombinant pmHS2 is thus also a heparosan synthase. As shown in the following Table XX, the Type F PmHS2 can incorporate the authentic heparin sugars.

Table XX
Activity of pmHS2 from Type F

Membranes	Acceptor	^{3}H-GlcNAc (dpm)	^{14}C-GlcUA (dpm)
Blank	0	8	8
PmHS2 F 3	+	7100	3100
PmHS2 F 4	0	6100	3800
PmHS2 F 4	+	11000	6400
PmHS2 F 18	0	20000	10000
PmHS2 F 18	+	23000	12000
PmHS2 D 7	0	36000	17000

[000216] The pmHS2 homolog of *P. multocida* Type F strain P-4218 was amplified with flanking primers as described for the Type A and D strains. The ORF was subcloned into the pETBlue-1 system in *E. coli* Tuner cells for use as a source of membrane preparations as described. Three independent clones (F 3,4,18) were assayed under standard HS assay

measuring radiolabeled sugar incorporation with paper chromatography. A negative control, membranes from "Blank" vector and a positive control, the Type D pmHS2 clone D7, were tested in parallel. Reactions plus/minus the Type D polymer acceptor were assayed.

[000217] The next best heterologous matches for the pmHS1 enzyme in the Genbank database are KfiA and KfiC proteins from *E. coli* K5; these two proteins work together to make the heparosan polymer. There is a good overall alignment of the enzyme sequences if smaller portions of pmHS1 ORF are aligned separately with KfiA (pmHS12, SEQ ID NO:63)and KfiC (pmHS11, SEQ ID NO:64) (FIG. 14). The MULTALIN alignment program (Corpet, 1988) identified regions that were very similar. Some of the most notable sequence similarities occur in the regions containing variants of the DXD amino acid sequence motif. Indeed, the first 1-360 residues of pmHS1 align with an approximate 38% identity to the *E. coli* KfiC, a single action GlcUA-transferase, while the 361-617 residues of pmHS12 align with an approximate 31% identity to the *E. coli* KfiA, a GlcNAc-transferase (FIG. 15). Thus, the pmHS1 is a naturally occurring fusion of two different glycosyltransferase domains. The pmHS1 is a dual action enzyme that alone makes heparin/heparosan polymers because both sugar transferase sites exist in one polypeptide enzyme.

[000218] The amino acid sequence of the heparosan synthase, pmHS1, however, is very different from other *Pasteurella* GAG synthases, pmHAS and pmCS. The pmHAS and pmHS1 enzymes both perform the task of polymerizing the identical monosaccharides; HA and heparin only differ with respect to their linkages. The creation of different anomeric linkages probably requires very distinct active sites due to the disparity between a retaining (to form α-linkages) and an inverting (to form β-linkages) transfer mechanism. The putative dual-action vertebrate heparin synthases, EXT1 (SEQ ID NO:65) and EXT 2 (SEQ ID NO:66), also appear to have two transferase domains, but the amino acid sequences are not similar to pmHS1. Thus, by aligning pmHS2, pmHS1 (B10 and A2 clones), KfiA, or KfiC, deduced amino acid sequence motifs have been identified. Such motifs are listed below and the alignment is shown in FIG. 15A-D.

[000219] Comparisons of the two known sets of heparin/heparosan biosynthesis enzymes from the *E. coli* K5 *Kfi* locus, the PmHS2 enzyme, and the pmHS1 from Type D capsular locus, allows for the initial assessment and bioinformatic prediction of new enzymes based on the amino acid sequence data. The closer the match (%identity) in a single polypeptide for the two sequence motifs described hereinafter (corresponding to the critical elements of the GlcUA-transferase and the GlcNAc-transferase), the higher the probability that the query enzyme is a new heparin/heparosan synthase (a single dual-action enzyme). The closer the match (%identity) in two polypeptides (especially if encoded in the same operon or transcriptional

unit) for the two sequence motifs, the higher the probability that the query enzymes are a pair of single-action glycosyltransferases. Thus, one of ordinary skill in the art would appreciate that given the following motifs, one would be able to ascertain and ascribe a probable heparin synthase function to a newly discovered enzyme and then test this ascribed function in a manner to confirm the enzymatic activity. Thus, single dual-action enzymes possessing enzymatic activity to produce heparin/heparosan and having at least one of the two disclosed motifs are contemplated as being encompassed by the presently claimed and disclosed invention.

[000220] Motif I: (SEQ ID NO:67)

QTYXN(L/I)EX_4DDX(S/T)(S/T)D(K/N)(T/S)X_6IAX(S/T)(S/T)(S/T)(K/R)V(K/R)X_6NXGXYX$_{16}$FQD XDDX(C/S)H(H/P)ERIXR

[000221] Motif II: (SEQ ID NO:68)

(K/R)DXGKFIX$_{12\text{-}17}$DDDI(R/I)YPXDYX$_3$MX$_{40\text{-}50}$ VNXLGTGTV

Motif I corresponds to the GlcUA transferase portion of the enzyme, while Motif II corresponds to the GlcNAc transferase portion of the enzyme. With respect to the motifs:

X = any residue

parentheses enclose a subset of potential residues [separated by a *slash*] that may be at a particular position (e.g. - (K/R) indicates that either K or R may be found at the position - i.e. there are semiconserved residues at that position.

[000222] The *consensus* X spacing is shown with the number of residues in *subscript* (e.g. $X_{12\text{-}17}$), but there are weaker constraints on these particular residues, thus spacing may be longer or shorter. Conserved residues may be slightly different in a few places especially if a chemically similar amino acid is substituted (*e.g.* K for a R, or E for a D). Overall, at the 90% match level, the confidence in this predictive method is very high, but even a 70-50% match level without excessive gap introduction (*e.g.* altered spacing between conserved residues) or rearrangements (miss-positioning with respect to order of appearance in the amino to carboxyl direction) would also be considered to be within the scope of these motifs. One of ordinary skill in the art, given the present specification, general knowledge of the art, as well as the extensive literature of sequence similarity and sequence statistics (*e.g.* the BLAST information website at www.ncbi.nlm.mih.gov), would appreciate the ability of a practitioner to identify potential new heparin/heparosan synthases based upon sequence similarity or adherence to the motifs

presented herein and thereafter test for functionality by means of heterozologous expression, to name but one example.

pmHS1 and PmHS2 Polymer Grafting and Use of Chimeric r Hybrid r Mutant Transferases.

[000223] As mentioned hereinabove, it was first discovered and disclosed that pmHAS-catalyzed synthesis *in vitro* was unique in comparison to all other existing HA synthases of *Streptococcus,* bacteria, humans or an algal virus. Specifically, recombinant pmHAS can elongate exogenously supplied functional acceptors (described herein) into longer glycosaminoglycans. The pmHAS synthase adds monosaccharides one at a time in a step-wise fashion to the growing chain. The pmHAS' exquisite sugar transfer specificity results in the repeating sugar backbone of the GAG chain. The pmCS enzyme, which is 90% identical at the amino acid level to pmHAS, performs the same synthesis reactions but incorporates GalNAc instead of GlcNAc. The pmHS1 and PmHS2 enzymes can also add heparosan chains onto exogenous supplied functional acceptors such as long or short heparosan polymers.

[000224] The *Pasteurella* GAG synthases (pmHAS, pmCS, pmHS1 and PmHS2) are very specific glycosyltransferases with respect to the sugar transfer reaction: usually only the authentic sugar is added onto acceptors. The epimers or closely structurally related molecules (*e.g.* UDP-glucose) are not utilized. However, these GAG synthases from *Pasteurella* do utilize heterologous acceptor sugars. For example, pmHAS elongates short chondroitin acceptors with HA chains. Additionally, pmHS1 adds heparosan chains onto HA acceptor oligosaccharides. Thus, a diverse range of hybrid of chimeric or hybrid GAG oligosaccharides can be made with the disclosed GAG synthases (i.e. pmHAS, pmCS, pmHS1, and PmHS2). The chemoenzymatic methodology can be used in either a liquid-phase synthesis of soluble, free sugars or in a solid-phase synthesis to build sugars on surfaces (as disclosed hereinafter).

[000225] Synthase activity assays (2.5 hours, 30°C) with subsequent paper chromatography separations and liquid scintillation counting of the origin zone. Typical reaction buffer (Tris & Mn ion; DeAngelis & White 2001) contained both radioactive UDP-GlcNAc and UDP-GlcUA and various acceptor sugars (as noted in table). Unless noted, the HA was from testicular Haase digestions (Leech means leech HAase). Hep2 or Hep2 are synthetic heparosan disaccharide or trisaccharide analogs, respectively (Haller & Boons, 2001). Recombinant *E. Coli* derived membranes from cell with plasmids containing pmHS1 gene or no insert (vector). With no membranes and no acceptor sugar, the background was 70 and 35 dpm, respectively.

TABLE XXI
Acc ptor Sugar Usage of pmHS1 Test

	PmHS1		Vect r	
Acceptor Sugar	**^{3}H-GlcNAc**	**^{14}C-GlcUA**	**^{3}H-GlcNAc**	**^{14}C-GlcUA**
	(dpm)		**(dpm)**	
None	690	580	55	60
Type D (0.38µg) sonicated	4400	4500	80	60
Heparin (10 µg) porcine	570	560	50	65
HA_4 (12.5 µg)	5900	6500	85	65
HA_4 (0.5 µg)	2200	2600	60	75
HA_{4-10} (25 µg)	7400	6900	75	70
HA_{4-10} (1 µg)	2300	2200	120	70
HA_4 leech (12.5 µg)	880	670	45	85
HA_{8-14} leech (25 µg)	1100	1000	70	90
Hep2 (1 µg)	1800	1700	70	95
Hep3 (25 µg)	5800	5600	55	75
Hep3 (1 µg)	9700	10000	45	90

[000226] Thus, chimeric or hybrid GAGS can be made using the *Pasteurella* GAG synthases of the presently claimed and disclosed invention. As shown in Table XXI, synthetic di- and tri-saccharides of heparosan, and HA can be elongated. Naturally derived HA tetramers can also be elongated. The reducing end is not required to be in a free state (aglycons are not a problem), therefore, the reducing end can serve as the tether site onto a surface, drug, or other synthetic or natural molecule. Exemplary compounds that can be made using the *Pasteurella* GAGs of the presently claimed and disclosed invention include, but are not limited to:

HA-C	CS-HA	C-HA	HA-HP C-HP	HA-C-HA
CS-HA-C	C-HA-C	HA-C-HP	CS-HA-HP	C-HA-HP

and so forth, and one of ordinary skill in the art given this specification would appreciate and be able to construct any number of chimeric or hybrid GAG molecules using the *Pasteurella* GAG synthases disclosed and claimed herein. With respect to the above-referenced chimeric or hybrid GAGs, HA=hyaluronan; C=chondroitin; CS=chondroitin sulfate; and HP=heparosan or heparin like molecules.

[000227] The C-terminal halves of pmHAS and pmCS (the putative GlcUA-transferase) can be switched and the sugar-transfer specificity for GlcNAc and GalNAc is not disturbed. This finding suggested that the hexosamine specificity determinants of the enzymes between GlcNAc- and GlcUA-transfer are located in their amino-terminal halves. To define the critical residues or regions that specify sugar transfer, further domain swapping were performed by PCR-overlap-extension (FIG. 16).

[000228] Certain chimeric or hybrid constructs, such as pm-EG and pm-IK (FIG. 16), are not dual-action enzymes and do not have either pmHAS nor pmCS activities. But pm-FH, which possesses pmCS residues 1-258, is an active pmCS, although its remaining part is from pmHAS residues 266-703. When more of the pmCS sequence is replaced by pmHAS sequence as in pm-JL enzyme construct (which possesses pmCS residues 1-214 at the amino-terminal and pmHAS residues 222-703 at the carboxyl-terminal), the enzyme is converted into a catalyst with HAS activity. The conversion of GalNAc-transferring activity into GlcNAc-transferring activity indicated that residues 222-265 of pmHAS and probably the corresponding residues 215-258 of pmCS play critical role in the selectivity between binding and/or transferring of GalNAc and GlcNAc substrate.

[000229] Site-directed mutagenesis of region HAS222-265/CS215-258: none of the residues tested in this region are sufficient alone to switch the sugar transfer specificity between pmHAS and pmCS. In the above identified regions, there are 14 residues that are different between pmHAS and pmCS. We checked the primary sequences of the predicted chondroitin synthases from several independent type F *Pasteurella multocida* in the region of 215to 258. Based on the comparison of these amino acid sequences, most of the differences between pmHAS and pmCS are conserved among those independent strains (FIG. 17). To identify possible critical individual residues that might be important for the selectivity between GalNAc and GlcNAc substrate, we utilized site-directed mutagenesis to change a single or multiple residues in this region. We used either $pmHAS^{1-703}$ DNA (for I243-, I243/G244/L245-containing mutants) or $pmCS^{1-704}$ DNA (for Y216-, L220-, or C221-containing mutants) as templates and replaced the target residue(s) with the corresponding one(s) in the other enzyme (FIG. 17). Results from enzymatic assays showed that all $pmCS^{1-704}$ mutants transfer GalNAc instead of GlcNAc and all $pmHAS^{1-703}$ mutants transfer GlcNAc instead of GalNAc. This finding

indicates that none of the residues that we tested here are sufficient alone to switch the sugar transfer specificity between pmHAS and pmCS.

D main swapping between pmHAS and pmCS: $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$ transfers both GlcNAc and GalNAc and GlcN.

[000230] Based on the above studies, we hypothesized that additional residues in the 44-residues region were important for the selectivity between GalNAc and GlcNAc transferase. To prove our hypothesis, this region was swapped between $pmHAS^{1-703}$ and $pmCS^{1-704}$ by PCR-overlap-extension. Pm-EG and pPmF4A (a library clone containing pmCS gene locus) DNAs were used to create $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$. Pm-FH and pPm7A (a c library clone containing pmHAS gene locus) DNAs were used to create $pmHAS^{1-221}$-$CS^{215-258}$-$HAS^{266-703}$ (FIG. 18). $PmHAS^{1-221}$-$CS^{215-258}$-$HAS^{266-703}$ did not express. Interestingly, $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$ could transfer both GlcNAc and GalNAc with preference for UDP-GalNAc as judged by HAS assay and CS assay, supporting our conclusion that this region in pmHAS and pmCS plays a critical role in determination of sugar substrate specificity. We also obtained a $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$ clone that possesses an additional mutation of I243V; this clone lost GlcNAc-transferring activity and was switched back into a chondroitin synthase. This finding suggests that I243 in pmHAS, and probably V236 in pmCS, plays important yet unknown roles in the determination of sugar substrate specificity.

[000231] In order to examine whether $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$ could transfer sugars other than GlcNAc and GalNAc, different sugar substrates, including UDP-glucose, UDP-galactose, UDP-mannose, UDP-xylose and UDP-glucosamine (GlcN), along with isotope-labeled GlcUA and HA oligosaccharide acceptor, were included when performing the polymerization assay. The results demonstrated that $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$ will use UDP-GlcNAc, UDP-GalNAc, or UDP-glucosamine Table XXII. This observation indicated that although swapping of the small region between pmCS and pmHAS resulted in relaxation of substrate selectivity, the enzyme is not so promiscuous that all UDP-sugars will substitute.

[000232] We exploited the possibility that the chimeric or hybrid enzyme could synthesize hybrid polymers with a blend of HA- and chondroitin-like sugars. We performed reactions containing ^{3}H-UDP-GalNAc, ^{14}C-UDP-GlcNAc, UDP-GlcUA and HA acceptor. The ratio of the incorporation of ^{3}H-GalNAc and ^{14}C-GlcNAc changed according to the UDP-sugar ratio in the reaction mixture included in the reaction. Gel filtration analysis of the polymerization products demonstrated that the molecules contain both ^{3}H and ^{14}C. The characterization of all the chimeric or hybrid proteins is summarized in FIG. 19.

Table XXII
Sugar substrate specificity of $pmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$

Standard polymerization assay were performed in the presence of isotope-labeled GlcUA, HA oligosaccharide acceptor, and one of the following sugar substrates. The sugar incorporation was indicated as the percentage of the incorporation of UDP-GalNAc. $PmCS^{1-214}$-$HAS^{222-265}$-$CS^{258-704}$ can transfer GalNAc, GlcNAc, and Glucosamine.

substrate sugar	incorporation
UDP-GalNAc	100%
UDP-GlcNAc	28%
UDP-Glucosamine	2%
UDP-Galactose	not detectable
UDP-Glucose	not detectable
UDP-Mannose	not detectable
UDP-Xylose	not detectable

[000233] Truncation analysis of pmHAS has identified a carboxyl-terminal region that appears to be responsible for the membrane association of pmHAS. Site-directed mutagenesis studies focused on several conserved motifs indicated that these conserved residues are critical for function. Evidence is provided that pmHAS and pmCS each contain two separate glycosyltransferase sites (FIG. 13). Thus the novel "one polypeptide, two active sites" theory has been confirmed. A 44-residue region of the enzymes has been demonstrated to be critical for sugar-transfer specificity. Based on this discovery, an enzyme that can transfer GalNAc, GlcN, and GlcNAc has been engineered.

[000234] Type A *Pasteurella multocida* produces a hyaluronan [HA] capsule to enhance infection. The 972-residue hyaluronan synthase, pmHAS, polymerizes the linear HA polysaccharide chain composed of GlcNAc and GlcUA. PmHAS possesses two separate glycosyltransferase sites. Protein truncation studies demonstrated that residues 1-117 can be deleted without affecting catalytic activity. The carboxyl-terminal boundary of the GlcUA-transferase resides within residues 686-703. Both sites contain a DXD motif. All four aspartate residues are essential for HA synthase activity. D247 and D249 mutants possessed only GlcUA-transferase activity while D527 and D529 mutants possessed only GlcNAc-transferase activity. These results further confirm our previous assignment of the active sites within the synthase polypeptide. The WGGED sequence motif appears to be involved in GlcNAc-transferase activity because E396 mutants and D370 mutants possessed only GlcUA-transferase activity.

[000235] Type F *P. multocida* synthesizes an unsulfated chondroitin GalNAc and GlcUA capsule. Domain swapping between pmHAS and the homologous chondroitin synthase, pmCS,

was performed. A chimeric or hybrid enzyme consisting of residues 1-427 of pmHAS and residues 421-704 of pmCS was an active HA synthase. On the other hand, the converse chimeric or hybrid enzyme consisting of residues 1-420 of pmCS and residues 428-703 of pmHAS was an active chondroitin synthase. Overall, these findings support the model of two independent transferase sites within a single polypeptide as well as further delineate the site boundaries.

[000236] pmHAS utilizes two separate glycosyltransferase sites to catalyze the transfer of GlcNAc and GlcUA to form the HA polymer. Within the pmHAS sequence, there is a pair of duplicated domains which are similar to the "Domain A" proposed by Saxena. Both domains of pmHAS possess a short sequence motif containing DGS that is conserved among many β-glycosyltransferases. Changing the aspartate in either motif to asparagines, glutamate, or lysine significantly reduced or eliminated the HAS activity. However, the D196 mutants and the D477 mutants maintain high level of GlcUA-transferase and GlcNAc-transferase activity, respectively.

[000237] pmCS contains 965 amino acid residues and is about 90% identical to pmHAS. A soluble recombinant *Escherichia coli*-derived $pmCS^{1-704}$ catalyzes the repetitive addition of sugars from UDP-GalNAc and UDP-GlcUA to chondroitin oligosaccharide acceptors *in vitro.*

[000238] In order to analyze the contribution of the amino terminal region of pmHAS, various recombinant truncated polypeptides were produced ($pmHAS^{46-703}$, $pmHAS^{72-703}$, $pmHAS^{96-703}$ and $pmHAS^{118-703}$) in *E. coli.* The truncated versions $pmHAS^{46-703}$ and $pmHAS^{72-703}$ were as active as $pmHAS^{1-703}$, a soluble polypeptide with complete HAS activity. $PmHAS^{96-703}$ expressed at a very low level compared with other constructs but was active. $PmHAS^{118-703}$ expressed better than $pmHAS^{96-703}$ and still elongated HA chains. Therefore, it is probable that further deletion beyond residue 72 affected the overall folding efficiency of the entire polypeptide. Observation of lower molecular weight degradation bands derived from $pmHAS^{118-703}$ on Western blots also suggests that improper folding occurs to some extent. Overall, these findings suggest that the amino-terminal 117 residues are not required for HA synthase activity.

[000239] $pmHAS^{1-650}$ loses its GlcUA-transferase activity. To further delineate the GlcUA-transferase domain within the carboxyl terminal region, two slightly longer mutants, $pmHAS^{1-668}$ and $pmHAS^{1-686}$ were created. Both mutants also could not polymerize HA due to the loss of GlcUA-transferase activity, indicating that the carboxyl-terminal boundary of the GlcUA-transferase resides between residues 686 and 703.

Monodisperse Glycosaminoglycan P lymer Synthesis

[000240] The size of the hyaluronan [HA] polysaccharide dictates its biological effect in many cellular and tissue systems based on many reports in the literature. However, no source of very defined, uniform HA polymers with sizes greater than 5 kDa is currently available. This situation is complicated by the observation that long and short HA polymers appear to have antagonistic or inverse effects on some biological systems. Therefore, HA preparations containing a mixture of both size populations may yield contradictory or paradoxical results. One embodiment of the novel method of the present invention produces HA with very narrow, monodisperse size distributions that are referred to herein as "selectHA."

[000241] The Pasteurella bacterial HA synthase enzyme, pmHAS, catalyzes the synthesis of HA polymers utilizing monosaccharides from UDP-sugar precursors *in vivo* and *in vitro*. pmHAS will also elongate exogenously supplied HA oligosaccharide acceptors *in vitro*; in fact, HA oligosaccharides substantially boost the overall incorporation rate. A purified recombinant, pmHAS derivative was employed herein to produce either native composition HA or derivatized HA.

[000242] HA polymers of a desired size were constructed by controlling stoichiometry (i.e. ratio of precursors and acceptor molecules). The polymerization process is synchronized in the presence of acceptor, thus all polymer products are very similar. In contrast, without the use of an acceptor, the polymer products are polydisperse in size. In the present examples, stoichiometrically controlled synchronized synthesis reactions yielded a variety of HA preparations in the range of ~15 kDa to about 1.5 MDa. Each specific size class had a polydispersity value in the range of 1.01 for polymers up to 0.5 MDa or ~1.2 for polymers of ~1.5 MDa (1 is the ideal monodisperse size distribution) as assessed by size exclusion chromatography/multi-angle laser light scattering analysis. The selectHA preparations migrate on electrophoretic gels (agarose or polyacrylamide) as very tight bands.

[000243] The use of a modified acceptor allows the synthesis of selectHA polymers containing radioactive (e.g. 3H, 125I), fluorescent (e.g. fluorescein, rhodamine), detection (i.e., NMR or X-ray), affinity (e.g. biotin) or medicant tags. In this scheme, each molecule has a single detection agent located at the reducing terminus. Alternatively, the use of radioactive UDP-sugar precursors allows the synthesis of uniformly labeled selectHA polymers with very high specific activities.

[000244] Overall, the selectHA reagents should assist in the elucidation of the numerous roles of HA in health and disease due to their monodisperse size distributions and defined compositions. It must be emphasized that unpredicted kinetic properties of the Pasteurella GAG synthases in a recombinant virgin state in the presence of defined, unnatural reaction

conditions facilitates targeted size range production of monodisperse polymers that are not synthesizable by previously reported methods.

[000245] Effect of HA acceptor on pmHAS-catalyzed polymerization. HA polymerization reactions were performed with purified pmHAS and UDP-sugar precursors under various conditions, and the reaction products were analyzed by agarose gel or acrylamide gel electrophoresis. The size distribution of HA products obtained were observed to be quite different based on the presence or absence of the HA4 acceptor in the reaction (Fig. 20A). When 30 mM of UDP-sugars were present as well as 0.03 ug/ul of HA4, pmHAS synthesized smaller chains with a narrow size distribution. The Mn determined by MALLS is 551.5kDa and its polydispersity (Mw/Mn) is 1.006 (Fig. 20B). However, without HA4, pmHAS synthesized a more polydisperse product with the same amount of precursor sugars. The Mn determined by MALLS is 1.53 MDa and its polydispersity (Mw/Mn) is 1.169.

[000246] To verify whether pmHAS can utilize HA acceptors of various sizes, parallel assays were set up using the same starting conditions, and at various times additional UDP-sugars were added to the reaction. The result indicated that intermediate products were utilized as starting material for later chain elongation by pmHAS. (Fig. 21).

[000247] Size control of HA. The polymerization by pmHAS in the presence of HA acceptor is a synchronized process, and thus a more defined HA preparation can be obtained with pmHAS. This synchronization is probably due to the difference in rate or efficiency of new chain initiation versus chain elongation as speculated earlier in DeAngelis, 199 and depicted in Fig. 22 model. The addition of acceptor appears to bypass the slower initiation step; thus all chains are elongated in parallel resulting in a more homogenous final population. A model demonstrating *Pasteurella* synthase reaction synchronization mediated by acceptor usage is shown in Fig. 23.

[000248] The synthase enzyme will preferentially add available UDP-sugar precursors to the acceptor termini. If there are many acceptors, thus many termini, then a limited amount of UDP-sugars will be distributed among many molecules and thus result in many short polymer chain extensions. Conversely, if there are few acceptors, thus few termini, then the limited amount of UDP-sugars will be distributed among few molecules and thus result in a few long polymer chain extensions (modeled in FIG. 24). It has previously been observed that chain initiation is the rate-limiting step for pmHAS, and the enzyme prefers to transfer sugars onto existing HA chains when acceptor is included in the reaction. If the polymerization is indeed a synchronized process, then the amount of HA4 should affect the final size of the HA product when the same amount of UDP-sugar is present. To test this speculation, assays were performed with various levels of HA4 with fixed amount of UDP-sugar and pmHAS (Fig. 25A).

To determine the size and polydispersity of these HA products, HA polymer sizes were determined by size exclusion chromatography - Multi Angle Laser Light Scattering (SEC-MALLS, Fig. 25B). Using the same strategy, HA was generated from 27 kDa to 1.3 MDa with polydispersity ranging from 1.001 to 1.2. Fig. 26 demonstrates the monodispersity of the various HA polymers resulting from reaction synchronization

[000249] *In vitro* synthesis of fluorescent HA. The *in vitro* technology for the production of monodisperse glycosaminoglycans also allows the use of modified acceptor to synthesize HA polymers containing various types of foreign moieties. An example is shown using fluorescent HA4 to produce fluorescent monodisperse HA of various sizes (Fig. 27). Similarly, radioactive (e.g. ^{3}H, ^{125}I), affinity (e.g. biotin), detection (e.g. probe for NMR or X-ray uses or a reporter enzyme), or medicant tagged glycosaminoglycan polymers are possible with the appropriate modified acceptor. However, the invention is not limited to the tags described herein, and other tags known to a person having ordinary skill in the art may be utilized in accordance with the present invention.

[000250] In addition to the small sugar chains (e.g. tetrasaccharide HA4), larger HA polymers can be used as starting acceptor for pmHAS; the enzyme will elongate existing chains with more sugars. Experiments were performed using 575 kDa HA and 970 kDa HA (synthesized *in vitro* with pmHAS and HA4 as acceptor, using the previously described methods) and a commercially available HA sample (~2 MDa; Genzyme) as acceptors. The results indicate that the existing HA chains were further elongated (FIG. 28). For example, the ~2 MDa starting material in lane 11 was elongated to produce the larger (i.e., slower migrating) material in lane 10. Therefore, a method for creating higher value longer polymers is also described by the present invention. The length of the final product can be controlled stoichiometrically as shown in lanes 7-9; a lower starting acceptor concentration (lane 7) results in longer chains because the same limited amount of UDP-sugars is consumed, making a few long chains instead of many shorter chains (lane 9).

[000251] The molecular weights of naturally existing HA polymers usually range from hundreds of thousands up to several millions of Daltons. For research requiring smaller HA polymers, enzymatic degradation is usually the first choice. However, this process is not satisfactory because it is time-consuming and the final yield of the targeted HA size fraction is low, and demanding chromatography is required. With the *in vitro* synthesis techniques of the present invention, HA as small as 10 kDa can be generated with polydispersity around 1.001.

[000252] High molecular HAs are commercially available from animal or bacterial sources. Problems with those include possible contaminants leading to immunological responses as well as broad size distribution (Soltes etc, 2002). Polydispersities (Mw/Mn) are

commonly higher than 1.5. Conclusions drawing from experimental data during biological research with these HA could be misleading. Thus there exists a need for uniform HA to perform biological study, as agreed by Uebelhart and Williams (1999).

[000253] To determine the exact average molecular mass of HA, MALLS is usually the choice. Yet many people have the need to quickly estimate the mass. For this purpose, some groups investigated the correlation of HA migration on agarose gel with DNA (Lee and Cowman, 1994). The drawback of this method is that, first, the HA samples used were not uniform, and second, the migration of HA and DNA on agarose gel changes differently with the change of the concentration of agarose gel. The *in vitro* generated HA of defined size distribution provide excellent series of standards for this purpose (Fig. 29).

[000254] In general, the unique technologies of the present invention allow the generation of a variety of defined, monodisperse HA tools for elucidating the numerous roles of HA in health and disease due to their monodisperse size distributions and defined compositions.

[000255] In addition to making HA polymers, the relaxed acceptor specificity of pmHAS allows the use of various chondroitin acceptors. This allows the production of monodisperse hybrid GAGs that have utility in medicine including tissue engineering and surgical aids. In particular, new protein-free proteoglycans are now possible that do not have antigenicity or allergenicity concerns compared to animal-derived products.

[000256] In FIG. 30, various monodisperse chondroitin sulfate HA hybrid GAGs are created by elongating a variety of chondroitin sulfates (A, B, and C) with pmHAS, thus adding HA chains. Various amounts of HA were added to the preparations (at various times during reaction as noted) by adding more UDP-sugars. For example, lanes 3-6 show hybrids with a constant amount of chondroitin sulfate and increasing HA chain lengths. The starting chondroitin sulfates stain weakly here, and the band position is marked with an arrow. Without the acceptor (lanes 23-26), no such defined bands are seen; after a long period, some HA polymer shows up (lane 26) which results from *de novo* initiation without acceptor.

[000257] In FIG. 31, chondroitin sulfate A was elongated with pmHAS, thus adding HA chains. Various amounts of HA were added to the preparations by controlling the level of chondroitin acceptor (thus changing the UDP-sugar/acceptor ratio) as well as adding more UDP-sugars during the reaction. By changing the UDP-sugar/acceptor ratio, stoichiometric control of the hybrid GAG size was demonstrated.

[000258] In addition to extension with a HA synthase, other GAG synthases may be used in the methods of the present invention. For example, a chondroitin synthase such as but not limited to pmCS can be used to elongate an existing chondroitin sulfate polymer or HA polymer

to produce defined hybrid GAG molecules of various structures. Again, these molecules may have use as surgical aids or tissue engineering scaffolds.

[000259] In FIG. 32, pmCS and UDP-GlcUA, UDP-GalNAc were reacted with either a 81 kDa HA acceptor (lanes 3-7) or no acceptor (lanes 9-13). Various lengths of chondroitin were added to the HA chains (at longer times with more UDP-sugars producing longer hybrid chains). Without the acceptor, no such defined bands were seen; after a long period, some long pure chondroitin polymer shows up which results from *de novo* initiation without acceptor.

[000260] In FIG. 33, Size exclusion (or gel filtration) chromatography analysis coupled with multi-angle laser light scattering detection confirms the monodisperse nature of polymers created by the present invention. In the FIG. 33A, HA (starting MW 81 kDa) extended with chondroitin chains using pmCS (same sample used in Fig 32, lane #7, overnight [O/N] extension) was analyzed; the material was 280,000 Mw and polydispersity (Mw/Mn) was 1.003 +/- 0.024. Chondroitin sulfate HA extended with HA chains using pmHAS (same sample used in Fig 30, lane #23) was analyzed and shown in FIG. 33B; the material was 427,000 Mw and polydispersity (Mw/Mn) was 1.006 +/- 0.024.

[000261] In FIG. 34 a 0.7% agarose gel detected with Stains-all compares the monodisperse, 'select HA' to commercially produced HA samples is shown. In lanes 1-3, the mixture of various monodisperse HAs made by the present invention (separate reaction products that were recombined to run all in one lane; sizes from top to bottom of lane: 1.27 MDa, 946 kDa, 575 kDa, 284 kDa, 27 kDa) run as discrete, tight bands. In contrast, in lanes 4-7, the commercially produced HA samples run as polydisperse smears (lane 4, 1.1 MDa; 5, 810 kDa; 6, 587 kDa; 7, 350 kDa). Remarkably, the monodisperse HA bands look almost as narrow as the single-molecule species of DNA present in lane 8 (BIOLINE standard).

Biomaterials and Methods of Making Same.

[000262] Biomaterials also play a pivotal role in the field of tissue engineering. Biomimetic synthetic polymers have been created to elicit specific cellular functions and to direct cell-cell interactions both in implants that are initially cell-free, which may serve as matrices to conduct tissue regeneration, and in implants to support cell transplantation. Biomimetic approaches have been based on polymers endowed with bioadhesive receptor-binding peptides and mono- and oligosaccharides. These materials have been patterned in two- and three-dimensions to generate model multicellular tissue architectures, and this approach may be useful in future efforts to generate complex organizations of multiple cell types. Natural polymers have also played an important role in these efforts, and recombinant polymers that combine the beneficial aspects of natural polymers with many of the desirable features of synthetic polymers have

been designed and produced. Biomaterials have been employed to conduct and accelerate otherwise naturally occurring phenomena, such as tissue regeneration in wound healing in the otherwise healthy subject; to induce cellular responses that might not be normally present, such as healing in a diseased subject or the generation of a new vascular bed to receive a subsequent cell transplant; and to block natural phenomena, such as the immune rejection of cell transplants from other species or the transmission of growth factor signals that stimulate scar formation.

[000263] Approximately 10 years ago, the concept of bioadhesion was introduced into the pharmaceutical literature and has since stimulated much research and development both in academia and in industry. The first generation of bioadhesive drug delivery systems (BBDS) were based on so-called mucoadhesive polymers, i.e. natural or synthetic macromolecules, often already well accepted and used as pharmaceutical excipients for other purposes, which show the remarkable ability to 'stick' to humid or wet mucosal tissue surfaces. While these novel dosage forms were mainly expected to allow for a possible prolongation, better localization or intensified contact to mucosal tissue surfaces, it had to be realized that these goals were often not so easily accomplished, at least not by means of such relatively straightforward technology. However, although not always convincing as a "glue", some of the mucoadhesive polymers were found to display other, possibly even more important biological activities, namely to inhibit proteolytic enzymes and/or to modulate the permeability of usually tight epithelial tissue barriers. Such features were found to be particularly useful in the context of peptide and protein drug delivery.

[000264] The primary goal of bioadhesive controlled drug delivery is to localize a delivery device within the body to enhance the drug absorption process in a site-specific manner. Bioadhesion is affected by the synergistic action of the biological environment, the properties of the polymeric controlled release device, and the presence of the drug itself. The delivery site and the device design are dictated by the drug's molecular structure and its pharmacological behavior.

[000265] One such bioadhesive known in the art is a fibrin "glue" and compositions which include one or more types of fibrin glue in combination with a medicament have been studied. For example, in order to test the effect on the handling properties of a two component fibrin glue, the viscosity of the fibrin glue was increased with sodium hyaluronate and the glue was applied to a microvascular anastomosis in rats. The femoral artery of each rat was anastomosed with three conventional sutures and then sealed with the fibrin glue. Three glues with different viscosities were tested: original Tisseel fibrin glue (Immuno AG, Vienna); Tisseel with 0.9% sodium chloride added to the fibrinogen component; and Tisseel with a high

molecular weight sodium hyaluronate (10 mg/ml, Healon, Pharmacia, Sweden) added to the fibrinogen component. The increased viscosity of the fibrin glue to which hyaluronate had been added resulted in a significantly higher patency rate 20 minutes after completion of the anastomosis ($p < 0.01$), and reduced the amount of fibrin that entered the vessels. Wadstrom et al. "Fibrin glue (Tisseel) added with sodium hyaluronate in microvascular anastomosing." Scand J Plast Reconstr Surg Hand Surg 1993 Dec;27(4):257-61.

[000266] The typical properties of the bioadhesive fibrin system described above ensue from its physiological properties. Filling the wound enhances natural biological processes of healing. The tissue reaction to the applied tissue fibrin coagulum is favorable. The treated parenchymatous organs, liver and spleen, heal with a smooth scar. The number of adhesions in the peritoneal cavity in all known treated experimental animals after treatment of the spleen was similar. Fewer adhesions are also observed when using a bioadhesive for repairing liver injuries in rabbits. The macroscopic appearance of the scar was similar, the scar was less visible in the liver parenchyma. The histological appearance was similar. The bioadhesive did not damage the tissue surrounding the parenchyma and did not act as a foreign body. These results confirm the biocompatibility of the fibrin glue as well as tissue tolerance and satisfactory healing without a reaction to the bioadhesive. After healing the bioadhesive is typically replaced by natural fibrous tissue.

[000267] Despite the effectiveness and successful use of the fibrin glue by medical practitioners in Europe, neither fibrin glue nor its essential component fibrinogen is widely used in the United States at the present time because of the general risks and problems of infection from pooled blood products contaminated with lipid-enveloped viruses such as HIV, associated with AIDS, and the hepatitis causing viruses such as HBV and HCV, as well as cytomegalovirus (CMV), Epstein-Barr virus, and the herpes simplex viruses in fibrinogen preparations. Thus, a naturally occurring or recombinantly produced bioadhesive which is not derived from pooled blood sources is actively being sought. The bioadhesive of the present invention fulfills such a need.

[000268] For example, one embodiment of the present invention is the use of sutures or bandages with HA-chains grafted on the surface or throughout the material in combination with the fibrinogen glue. The immobilized HA does not diffuse away as in current formulations, but rather remains at the wound site to enhance and stimulate healing.

[000269] Organic materials have also been postulated for use as bioadhesives. Bioadhesive lattices of water-swollen poly(acrylic acid) nano-and microparticles have been synthesized using an inverse (W/O) emulsion polymerization method. They are stabilized by a co-emulsifier system consisting of SpanTM 80 and TweenTM 80 dispersed in aliphatic

hydrocarbons. The initial polymerization medium contains emulsion droplets and inverse micelles which solubilize a part of the monomer solution. The polymerization is then initiated by free radicals, and particle dispersions with a narrow size distribution are obtained. The particle size is dependent on the type of radical initiator used. With water-soluble initiators, for example ammonium persulfate, microparticles are obtained in the size range of 1 to 10 micrometer, indicating that these microparticles originate from the emulsion droplets since the droplet sizes of the W/O emulsion show similar distribution. When lipophilic radical initiators, such as azobis-isobutyronitrile, are used, almost exclusively nanoparticles are generated with diameters in the range of 80 to 150 nm, due to the limited solubility of oligomeric poly(acrylic acid) chains in the lipophilic continuous phase. These poly(acrylic acid) micro- and nanoparticles yielded excellent bioadhesive properties in an in-vitro assay and may, therefore, be suitable for the encapsulation of peptides and other hydrophilic drugs.

[000270] In the present invention, HA or chondroitin chains would be the natural substitute for poly(acrylic-acid) based materials. HA is a negatively-charged polymer as is poly(acrylic-acid), but HA is a naturally occurring molecule in the vertebrate body and would not invoke an immune response like a poly(acrylic-acid) material.

[000271] The interest in realizing 'true' bioadhesion continues: instead of mucoadhesive polymers, plant or bacterial lectins, i.e. adhesion molecules which specifically bind to sugar moieties of the epithelial cell membrane, are now widely being investigated as drug delivery adjuvants. These second-generation bioadhesives not only provide for cellular binding, but also for subsequent endo- and transcytosis. This makes the novel, specifically bioadhesive molecules particularly interesting for the controlled delivery of DNA/RNA molecules in the context of antisense or gene therapy.

[000272] For the efficient delivery of peptides, proteins, and other biopharmaceuticals by nonparenteral routes, in particular via the gastrointestinal, or GI, tract, novel concepts are needed to overcome significant enzymatic and diffusional barriers. In this context, bioadhesion technologies offer some new perspectives. The original idea of oral bioadhesive drug delivery systems was to prolong and/or to intensify the contact between controlled-release dosage forms and the stomach or gut mucosa. However, the results obtained during the past decade using existing pharmaceutical polymers for such purposes were rather disappointing. The encountered difficulties were mainly related to the physiological peculiarities of GI mucus. Nevertheless, research in this area has also shed new light on the potential of mucoadhesive polymers. First, one important class of mucoadhesive polymers, poly(acrylic acid), could be identified as a potent inhibitor of proteolytic enzymes. Second, there is increasing evidence that the interaction between various types of bio(muco)adhesive polymers and epithelial cells has direct influence

on the permeability of mucosal epithelia. Rather than being just adhesives, mucoadhesive polymers may therefore be considered as a novel class of multifunctional macromolecules with a number of desirable properties for their use as biologically active drug delivery adjuvants.

[000273] In the present invention, HA or other glycosaminoglycan polysaccharides are used. As HA is known to interact with numerous proteins (i.e. RHAMM, CD44) found throughout the healthy and diseased body, then naturally occurring adhesive interactions can be utilized to effect targeting, stabilization, or other pharmacological parameters. Similarly, chondroitin interacts with a different subset of proteins (i.e. platelet factor 4, thrombin); it is likely that this polymer will yield properties distinct from HA and widen the horizon of this technology.

[000274] In order to overcome the problems related to GI mucus and to allow longer lasting fixation within the GI lumen, bioadhesion probably may be better achieved using specific bioadhesive molecules. Ideally, these bind to surface structures of the epithelial cells themselves rather than to mucus by receptor-ligand-like interactions. Such compounds possibly can be found in the future among plant lectins, novel synthetic polymers, and bacterial or viral adhesion/invasion factors. Apart from the plain fixation of drug carriers within the GI lumen, direct bioadhesive contact to the apical cell membrane possibly can be used to induce active transport processes by membrane-derived vesicles (endo- and transcytosis). The nonspecific interaction between epithelia and some mucoadhesive polymers induces a temporary loosening of the tight intercellular junctions, which is suitable for the rapid absorption of smaller peptide drugs along the paracellular pathway. In contrast, specific endo- and transcytosis may ultimately allow the selectively enhanced transport of very large bioactive molecules (polypeptides, polysaccharides, or polynucleotides) or drug carriers across tight clusters of polarized epi- or endothelial cells, whereas the formidable barrier function of such tissues against all other solutes remains intact.

[000275] Bioadhesive systems are presently playing a major role in the medical and biological fields because of their ability to maintain a dosage form at a precise body-site for a prolonged period of time over which the active principle is progressively released. Additional uses for bioadhesives include: bioadhesives/mucoadhesives in drug delivery to the gastrointestinal tract; nanoparticles as a gastroadhesive drug delivery system; mucoadhesive buccal patches for peptide delivery; bioadhesive dosage forms for buccal/gingival administration; semisolid dosage forms as buccal bioadhesives; bioadhesive dosage forms for nasal administration; ocular bioadhesive delivery systems; nanoparticles as bioadhesive ocular drug delivery systems; and bioadhesive dosage forms for vaginal and intrauterine applications.

[000276] The bioadhesive may also contain liposomes. Liposomes are unilamellar or multilamellar lipid vesicles which entrap a significant fraction of aqueous solution. The vesicular

microreservoirs of liposomes can contain a variety of water-soluble materials, which are thus suspended within the emulsion. The preparation of liposomes and the variety of uses of liposomes in biological systems has been disclosed in U.S. Patent Nos. 4,708,861, 4,224,179, and 4,235,871. Liposomes are generally formed by mixing long chain carboxylic acids, amines, and cholesterol, as well as phospholipids, in aqueous buffers. The organic components spontaneously form multilamellar bilayer structures called liposomes. Depending on their composition and storage conditions, liposomes exhibit varying stabilities. Liposomes serve as models of cell membranes and also are used as drug delivery systems.

[000277] Most attempts to use liposomes as drug delivery vehicles have envisioned liposomes as entities which circulate in blood, to be taken up by certain cells or tissues in which their degradation would slowly release their internal aqueous drug-containing contents. In an effort to aid in their up-take by a given target tissue, some liposomes have been Atailored@ by binding specific antibodies or antigens to the outer surface. Liposomes have also been devised as controlled release systems for the delivery of their contents in vivo. Compositions in which liposomes containing biologically active agents are maintained and immobilized in polymer matrices, such as methylcellulose, collagen and agarose, for sustained release of the liposome contents, are described in U.S. Patent No. 4,708,861 to Popescu et al.

[000278] In this manner, the present invention contemplates a bioadhesive comprising HA or chondroitin or heparin produced from pmHAS, pmCS, pmHS1, or PmHS2. The present invention also contemplates a composition containing a bioadhesive comprising HA or chondroitin or heparin produced from pmHAS, pmCS, pmHS1, or PmHS2 and an effective amount of a medicament, wherein the medicament can be entrapped or grafted directly within the HA or chondroitin or heparin bioadhesive or be suspended within a liposome which is entrapped or grafted within the HA or chondroitin or heparin bioadhesive. These compositions are especially suited to the controlled release of medicaments.

[000279] Such compositions are useful on the tissues, skin, and mucus membranes (mucosa) of an animal body, such as that of a human, to which the compositions adhere. The compositions so adhered to the mucosa, skin, or other tissue slowly release the treating agent to the contacted body area for relatively long periods of time, and cause the treating agent to be sorbed (absorbed or adsorbed) at least at the vicinity of the contacted body area. Such time periods are longer than the time of release for a similar composition that does not include the HA bioadhesive.

[000280] The treating agents useful herein are selected generally from the classes of medicinal agents and cosmetic agents. Substantially any agent of these two classes of materials that is a solid at ambient temperatures may be used in a composition or method of

the present invention. Treating agents that are liquid at ambient temperatures, e.g. nitroglycerine, can be used in a composition of this invention, but are not preferred because of the difficulties presented in their formulation. The treating agent may be used singly or as a mixture of two or more such agents.

[000281] One or more adjuvants may also be included with a treating agent, and when so used, an adjuvant is included in the meaning of the phrase "treating agent" or "medicament." Exemplary of useful adjuvants are chelating agents such as EDTA that bind calcium ions and assist in passage of medicinal agents through the mucosa and into the blood stream. Another illustrative group of adjuvants are the quaternary nitrogen-containing compounds such as benzalkonium chloride that also assist medicinal agents in passing through the mucosa and into the blood stream.

[000282] The treating agent is present in the compositions of this invention in an amount that is sufficient to prevent, cure and/or treat a condition for a desired period of time for which the composition of this invention is to be administered, and such an amount is referred herein as "an effective amount." As is well known, particularly in the medicinal arts, effective amounts of medicinal agents vary with the particular agent involved, the condition being treated and the rate at which the composition containing the medicinal agent is eliminated from the body, as well as varying with the animal in which it is being used, and the body weight of that animal. Consequently, effective amounts of treating agents may not be defined for each agent. Thus, an effective amount is that amount which in a composition of this invention provides a sufficient amount of the treating agent to provide the requisite activity of treating agent in or on the body of the treated animal for the desired period of time, and is typically less than that amount usually used.

[000283] Inasmuch as amounts of particular treating agents in the blood stream that are suitable for treating particular conditions are generally known, as are suitable amounts of treating agents used in cosmetics, it is a relatively easy laboratory task to formulate a series of controlled release compositions of this invention containing a range of such treating agent for a particular composition of this invention.

[000284] The second principle ingredient of this embodiment of the present invention is a bioadhesive comprising an amount of hyaluronic acid (HA) from pmHAS or chondroitin from PmCS or heparin from pmHS1 or PmHS2. Such a glycosaminoglycan bioadhesive made from a HA or chondroitin or heparin chain directly polymerized onto a molecule with the desired pharmacological property or a HA or chondroitin or heparin chain polymerized onto a matrix or liposome which in turn contains or binds the medicament.

[000285] Woodfield et al. (2002) describe that articular cartilage lesions resulting from trauma or degenerative diseases are commonly encountered clinical problems. It is well-established that adult articular cartilage has limited regenerative capacity, and, although numerous treatment protocols are currently employed clinically, few approaches exist that are capable of consistently restoring long-term function to damaged articular cartilage. Tissue engineering strategies that focus on the use of three-dimensional scaffolds for repairing articular cartilage lesions offer many advantages over current treatment strategies. Appropriate design of biodegradable scaffold conduits (either preformed or injectable) allow for the delivery of reparative cells bioactive factors, or gene factors to the defect site in an organized manner. This review seeks to highlight pertinent design considerations and limitations related to the development, material selection, and processing of scaffolds for articular cartilage tissue engineering, evidenced over the last decade. In particular, considerations for novel repair strategies that use scaffolds in combination with controlled release of bioactive factors or gene therapy.

[000286] The various glycosaminoglycans produced by the methods of the present invention, especially the hybrid or chimeric polymers, are promising materials for incorporation , either directly or indirectly, into a scaffold for cell growth and implantation. In addition, the polymers may be attached to surfaces or devices via acceptor moiety or a direct chain interaction.

[000287] Bello et al. (2001) describe that tissue-engineered skin is a significant advance in the field of wound healing and was developed due to limitations associated with the use of autografts. These limitations include the creation of a donor site which is at risk of developing pain, scarring, infection and/or slow healing. A number of products are commercially available and many others are in development. Cultured epidermal autografts can provide permanent coverage of large area from a skin biopsy. However, 3 weeks are needed for graft cultivation. Cultured epidermal allografts are available immediately and no biopsy is necessary. They can be cryopreserved and banked, but are not currently commercially available. A nonliving allogeneic acellular dermal matrix with intact basement membrane complex (Alloderm) is immunologically inert. It prepares the wound bed for grafting allowing improved cultured allograft 'take' and provides an intact basement membrane. A nonliving extracellular matrix of collagen and chondroitin-6-sulfate with silicone backing (Integra) serves to generate neodermis. A collagen and glycosaminoglycan dermal matrix inoculated with autologous fibroblasts and keratinocytes has been investigated but is not commercially available. It requires 3 to 4 weeks for cultivation. Dermagraft consists of living allogeneic dermal fibroblasts grown on degradable scaffold. It has good resistance to tearing. An extracellular matrix generated by allogeneic

human dermal fibroblasts (TransCyte) serves as a matrix for neodermis generation. Apligraf is a living allogeneic bilayered construct containing keratinocytes, fibroblasts and bovine type I collagen. It can be used on an outpatient basis and avoids the need for a donor site wound. Another living skin equivalent, composite cultured skin (OrCel), consists of allogeneic fibroblasts and keratinocytes seeded on opposite sides of bilayered matrix of bovine collagen. There are limited clinical data available for this product, but large clinical trials are ongoing. Limited data are also available for 2 types of dressing material derived from pigs: porcine small intestinal submucosa acellular collagen matrix (Oasis) and an acellular xenogeneic collagen matrix (E-Z-Derm). Both products have a long shelf life. Other novel skin substitutes are being investigated. The potential risks and benefits of using tissue-engineered skin need to be further evaluated in clinical trials but it is obvious that they offer a new option for the treatment of wounds.

[000288] The various glycosaminoglycans produced by the methods of the present invention, especially the hybrid or chimeric polymers, are promising components for tissue engineered organs including skin.

[000289] Vlodavsky et al. (1996) disclose that heparan sulfate proteoglycans (HSPGs) are ubiquitous macromolecules associated with the cell surface and extracellular matrix (ECM) of a wide range of cells of vertebrate and invertebrate tissues. The basic HSPG structure consists of a protein core to which several linear heparan sulfate (HS) chains are covalently attached. The polysaccharide chains are typically composed of repeating hexuronic and D-glucosamine disaccharide units that are substituted to a varying extent with N- and O-linked sulfate moieties and N-linked acetyl groups. Beside serving as a scaffold for the attachment of various ECM components (e.g., collagen, laminin, fibronectin), the binding of HS to certain proteins has been suggested to induce a conformational change which may lead to the exposure of novel reactive determinants or conversely stabilize an inert protein configuration. Of particular significance is the interaction of HS with fibroblast growth factors (FGFs), mediating their sequestration, stabilization and high affinity receptor binding and signaling. Cellular responses to FGFs may hence be modulated by metabolic inhibitors of HS synthesis and sulfation, HS-degrading enzymes, and synthetic mimetics of heparin/HS. HS is involved in basic FGF (bFGF) receptor binding and mitogenic activity and its modulation by species of heparin, HS, and synthetic polyanionic 'heparin-mimicking' compounds. The results are discussed in relation to the current thoughts on the dual involvement of low and high affinity receptor sites in the growth promoting and angiogenic activities of bFGF and other heparin-binding growth factors.

[000290] The mimetics based on the various glycosaminoglycans produced by the methods of the present invention, including the hybrid or chimeric polymers, are promising due to their

inherent abilities to interact, trigger, or bind a variety of molecules including cytokines, receptors, and growth factors. These GAG molecules should thus serve as modulators of cell behavior and/or growth via numerous natural pathways in mammals and humans.

[000291] Iivanainen et al. (2003) disclose that dynamic interactions between endothelial cells and components of their surrounding extracellular matrix are necessary for the invasion, migration, and survival of endothelial cells during angiogenesis. These interactions are mediated by matrix receptors that initiate intracellular signaling cascades in response to binding to specific extracellular matrix molecules. The interactions between endothelial cells and their environment are also modulated by enzymes that degrade different matrix components and thus enable endothelial invasion. Recent reports on gene targeting in mice have confirmed the role of two classes of matrix receptors, integrins and cell surface heparan sulfate proteoglycans, and a group of matrix degrading proteolytic enzymes, matrix metalloproteinases, in angiogenesis. The significance of endothelial cell-matrix interactions is further supported by several ongoing clinical trials that analyze the effects of drugs blocking this interaction on angiogenesis-dependent growth of human tumors.

[000292] The mimetics based on various glycosaminoglycans produced by the methods of the present invention, including the hybrid or chimeric polymers, are promising due to their inherent abilities to intearct, trigger, or bind a variety of molecules including cytokines, receptors, and growth factors. These molecules should thus serve as modulators of cell behavior and/or growth.

[000293] Song et al. (2002) teach that glypicans are a family of heparan sulfate proteoglycans that are bound to the cell surface by a glycosyl-phosphatidylinositol anchor. Six members of this family have been identified in mammals. In general, glypicans are highly expressed during development, and their expression pattern suggests that they are involved in morphogenesis. One member of this family, glypican-3, is mutated in the Simpson-Golabi-Behmel syndrome. This syndrome is characterized by overgrowth and various developmental abnormalities that indicate that glypican-3 inhibits proliferation and cell survival in the embryo. It has consequently been proposed that glypicans can regulate the activity of several growth factors that play a critical role in morphogenesis.

[000294] The various glycosaminoglycans produced by the methods of the present invention, especially the hybrid or chimeric polymers, are promising materials for incorporation, either directly or indirectly, onto cell surfaces. The polymers may be attached to cell surfaces or devices via acceptor moiety (for example, but not by way of limitation, a lipid conjugate).

MATERIALS AND METHODS

[000295] Membrane preparations containing recombinant pmHAS (GenBank AF036004) (SEQ. ID NOS: 1 and 2) were isolated from *E. coli* SURE(pPmHAS). Membrane preparations containing native pmHAS were obtained from the *P. multocida* strain P-1059 (ATCC #15742). pmHAS was assayed in 50 mM Tris, pH 7.2, 20 mM $MnC1_2$, and UDP-sugars (UDP-[^{14}C]GlcUA, 0.3 μCi/mmol, NEN and UDP-GlcNAc) at 30°C. The reaction products were analyzed by various chromatographic methods as described below. Membrane preparations containing other recombinant HAS enzymes, Group A *streptococcal* HasA or *Xenopus* DG42 produced in the yeast *Saccharomyces cerevisiae*, were prepared.

[000296] Uronic acid was quantitated by the carbazole method. Even-numbered HA oligosaccharides [$(GlcNAc\text{-}GlcUA)_n$] were generated by degradation of HA (from Group A *Streptococcus*) with either bovine testicular hyaluronidase Type V (n=2-5) or *Streptomyces hyaluroniticus* HA lyase (n=2 or 3) in 30 mM sodium acetate, pH 5.2, at 30°C overnight. The latter enzyme employs an elimination mechanism to cleave the chain resulting in an unsaturated GlcUA residue at the nonreducing terminus of each fragment. For further purification and desalting, some preparations were subjected to gel filtration with P-2 resin (BioRad) in 0.2 M ammonium formate and lyophilization. Odd-numbered HA oligosaccharides [$GlcNAc(GlcUA\text{-}GlcNAc)_n$] ending in a GlcNAc residue were prepared by mercuric acetate-treatment of partial HA digests generated by HA lyase (n=2-7). The masses of the HA oligosaccharides were verified by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. Sugars in water were mixed with an equal volume of 5 mg/ml 6-azo-2-thiothymine in 50% acetonitrile/0.1% trifluoroacetic acid, and rapidly air-dried on the target plate. The negative ions produced by pulsed nitrogen laser irradiation were analyzed in linear mode (20 kV acceleration; Perceptive Voyager).

[000297] Other oligosaccharides that are structurally similar to HA were also tested in HAS assays. The structure of heparosan pentamer derived from the *E. coli* K5 capsular polysaccharide is β4GlcUA-α4GlcNAc; this carbohydrate has the same composition as HA but the glycosidic linkages between the monosaccharides are different. The chitin-derived oligosaccharides, chitotetraose and chitopentaose, are β4GlcNAc polymers made of 4 or 5 monosaccharides, respectively.

[000298] Various oligosaccharides were radiolabeled by reduction with 4 to 6 equivalents of sodium borotritide (20 mM, NEN; 0.2 μCi/mmol) in 15 mM NaOH at 30°C for 2 hrs. ^{3}H-oligosaccharides were desalted on a P-2 column in 0.2 M ammonium formate to remove unincorporated tritium and lyophilized. Some labeled oligosaccharides were further purified preparatively by paper chromatography with Whatman 1 developed in pyridine/ethyl acetate/acetic acid/H_2O (5:5:1:3) before use as an acceptor.

[000299] Paper chromatography with Whatman 3M developed in ethanol /1M ammonium acetate, pH 5.5 (65:35) was used to separate high molecular weight HA product (which remains at the origin) from UDP-sugars and small acceptor oligosaccharides. In the conventional HAS assay, radioactive UDP-sugars are polymerized into HA. To obtain the size distribution of the HA polymerization products, some samples were also separated by gel filtration chromatography with Sephacryl S-200 (Pharmacia) columns in 0.2 M NaCl, 5 mM Tris, pH 8. Columns were calibrated with dextran standards. The identity of the polymer products was assessed by sensitivity to specific HA lyase and the requirement for the simultaneous presence of both UDP-sugar precursors during the reaction. Thin layer chromatography [TLC] on high performance silica plates with application zones (Whatman) utilizing butanol/acetic acid/water (1.5:1:1 or 1.25:1:1) development solvent separated ^{3}H-labeled oligosaccharides in reaction mixes. Radioactive molecules were visualized after impregnation with EnHance spray (NEN) and fluorography at ~80°C.

[000300] Membrane preparations containing recombinant full length pmHAS, pmHAS$^{437-972}$, pmHAS$^{437-756}$, pmHAS$^{1-756}$, pmHAS$^{1-567}$ and pmHAS$^{152-756}$ were isolated from *E. coli* as described. For soluble truncated pmHAS proteins, pmHAS$^{1-703}$, pmHAS$^{1-650}$, and pmHAS$^{1-703}$-derived mutants, cells were extracted with B-Per™ II Bacterial Protein Extraction Reagent (Pierce) according to the manufacturer's instruction except that the procedure was performed at 7°C in the presence of protease inhibitors. Membrane preparations of *P. multocida* P-1059 (ATCC 15742) were made as described. In order to test whether the truncated recombinant polypeptides were formed as insoluble inclusion bodies, membrane preparations were suspended in RIPA buffer (1% NP-40, 1% sodium deoxycholate and 0.1% SDS in 50 mM Tris, pH 7.2) for 20 minutes at room temperature. After centrifugation at 20,000 x *g* for 10 minutes, the supernatants were saved and the pellets were resuspended in RIPA buffer. The supernatants and the pellets were analyzed by SDS-polyacrylamide gel electrophoresis and Western blot analysis as described later.

[000301] Membranes and extracts were analyzed using standard 8% polyacrylamide SDS gels. Following electrophoresis, proteins were transferred with a semi-dry apparatus to nitrocellulose membranes (S&S) and detected with a monospecific antibody directed against a synthetic peptide corresponding to residues 526 to 543 of pmHAS. The peptide, acetyl-LDSDDYLEPDAVELCLKE-amide (SEQ ID NO: 22) (Quantum), was coupled to ovalbumin to form the initial immunogen for injection into female New Zealand white rabbits (HTI Bioscience protocols). In the subsequent boosts, free peptide was utilized. The specific antipeptide IgG was purified from ammonium sulfate fractionated sera (after third boost) using an immobilized peptide column (internal cysteine coupled to Iodoacetyl beads; Pierce). The desired IgG was

eluted with 0.1 M glycine, pH 2.5, neutralized, and exchanged into phosphate-buffered saline. Immunoreactive bands on Western blots were detected with a protein A-alkaline phosphatase conjugate and were visualized with 5-bromo-4-chloro-3-indolyl phosphate and nitroblue tetrazolium reagent.

[000302] The size of HA polymers was analyzed by chromatography on a Phenomenex PolySep-GFC-P 3000, P 4000 or P5000 column (300x7.8 mm) eluted with 0.2 M sodium nitrate at 0.6 ml/min on a Waters 600E system. The column was standardized with various size fluorescent dextrans (580, 50, and 12 kDa). Radioactive components were detected with a LB508 Radioflow Detector (EG & G Berthold) and Zinsser cocktail (1.8 ml/min). In comparison to the full HAS assay using paper chromatography described above, these 3 minute reactions contained twice the UDP-sugar concentrations, 0.06 µCi UDP-[^{14}C]GlcUA, and 0.25 µg even-numbered HA oligosaccharide. Also, addition of ethylenediamine tetracetic acid (final conc. 22 mM) and boiling (2 min) was employed to terminate the reactions instead of addition of SDS.

[000303] A lambda library of Sau3A partially digested Type F *P. multocida* P-4679 DNA (~4-9 kb average length insert) was made using the BamHI-cleaved "Zap Express" vector system (Stratagene). The plaque lifts were screened by hybridization (5x SSC, 50°C; 16 hrs) with the digoxigenin-labeled probe using the manufacturer guidelines for colorimetric development. *E. coli* XLI-Blue MRF' was co-infected with the purified, individual positive lambda clones and ExAssist helper phage to yield phagemids. The resulting phagemids were transfected into *E. coli* XLOLR cells to recover the plasmids. Sequence analysis of the plasmids revealed a novel open reading frame, which we called pmCS, with high homology to pmHAS.

[000304] In previous studies with pmHAS, it was found that a functional, soluble enzyme would be created if a portion of the carboxyl terminus was truncated by molecular genetic means. Therefore, a portion of the pmCS ORF (residues 1-704) in the insert of one of the excised lambda clones, pPmF4A, was amplified by 20 cycles of PCR with Taq polymerase. The sense primer corresponded to the sequence at the deduced amino terminus of the ORF and the antisense primer encoded the new carboxyl terminus followed by an artificial stop codon. The resulting PCR product was purified and concentrated using GeneClean. This insert was cloned using the pETBlue-1 Acceptor system (Novagen) according to the manufacturer's instructions. The Taq-generated single A overhang is used to facilitate the cloning of the open reading frame downstream of the T7 promoter and the ribosome binding site of the vector. The ligated products were transformed into *E. coli* NovaBlue and plated on LB carbenicillin (50 µg/ml) under conditions for blue/white screening. White or light blue colonies were analyzed by restriction digestion. A clone containing a plasmid with the desired truncated ORF, pPm-CS$^{1-704}$, was

transformed into *E. coli* Tuner, the T7 RNA polymerase-containing expression host, and maintained on LB media with carbenicillin and chloramphenicol (34 µg/ml) at 30°C. Log phase cultures were induced with β-isopropylthiogalactoside (0.2 mM final) for 5 hrs. The cells were harvested by centrifugation, frozen, and extracted for 20 min with a mild detergent (bPer II reagent, Pierce) at 7°C in the presence of a broad-range protease inhibitor cocktail. The cells were removed by centrifugation and the soluble extract was used as the source of CS enzyme for *in vitro* assays.

[000305] Truncated polypeptides were generated by amplifying the pPm7A insert by 13 cycles of PCR with Taq polymerase (Fisher) and synthetic oligonucleotide primers corresponding to various portions of the pmHAS open reading frame. Except for the construction of $pmHAS^{1-686}$ and $pmHAS^{1-668}$, the primers contained EcoRI and PstI restriction sites to facilitate cloning into the expression plasmid pKK223-3 (tac promoter; Pharmacia). The resulting recombinant constructs were transformed into E. coli TOP 10F' cells (Invitrogen) and maintained on Luria-Bertani media with ampicillin selection. The DNA encoding $pmHAS^{1-686}$ and $pmHAS^{1-668}$ were cloned into pETBlue-1 plasmid and expressed in Tuner (DE3)pLacI cells (Novagen) according to manufacturing instructions; these cells were maintained on Luria-Bertani media with carbenicillin and chloramphenicol selection.

[000306] Point mutations were made using the QuickChange site-directed mutagenesis method (Stratagene) with the plasmid pKK223/$pmHAS^{1-703}$ DNA as template. The sequences of the mutant open reading frames were verified by automated DNA sequencing (Oklahoma State University Recombinant DNA/Protein Resource Facility).

[000307] Recombinant *E. coli* were grown in Luria-Bertani media with drug selection until OD_{600} was 0.3-0.6 when cells were induced with 0.5 mM isopropyl-1-thio-β-D-galactoside. Cells were harvested 5 hours after induction. For soluble truncated proteins and $pmHAS^{1-703}$-derived mutants expressed in E. coli TOP10F' cell, cells were extracted with B-Per™ II Bacterial Protein Extraction Reagent (an octylthioglucoside-based solution; Pierce) according to the manufacturer's instruction except that the procedure was performed at 7°C in the presence of protease inhibitors. For proteins expressed in Tuner(DE3)pLacI, lysis by ultrasonication followed by subcellular fractionation was performed and the supernatant after centrifugation at 100,000 x g was used.

[000308] Five assays were designed to detect either (a) the polymerization of long HA chains, (b) the addition of a single GlcNAc to a GlcUA-terminated HA oligosaccharide acceptor, (c) the addition of a single GlcUA to a GlcNAc-terminated HA oligosaccharide acceptor, (d) the polymerization of long chondroitin chains, or (e) the addition of a single GalNAc to a GlcUA-terminated HA oligosaccharide acceptor. The first three assays were described

hereinabove. For the chondroitin synthase assay, the same conditions as the HA synthase assay were used except that the other hexosamine precursor, UDP-GalNAc, was employed and there is no ammonium sulfate or ethylene glycol in the assay system. GalNAc-transferase activity was assayed under the same conditions as the GlcNAc-transferase assay except that 0.3 mM UDP-[^{3}H]GalNAc (0.2 µCi; NEN) was used instead of UDP-[^{3}H]GlcNAc. Reactions were terminated by the addition of SDS to 2% (w/v). The reaction products were separated from substrates by descending paper (Whatman 3M) chromatography with ethanol/1 M ammonium acetate, pH 5.5, development solvent (65:35 for the HAS, chondroitin synthase, and GlcUA-transferase assays; 75:25 for GlcNAc-transferase and GalNAc-transferase assay). All assays were adjusted to be linear with regard to incubation time and to protein concentration. Radiolabeled products were quantitated by liquid scintillation counting (Biosafe II, Research Products International).

[000309] The pmHAS polypeptides in membranes and extracts were analyzed using standard 8% polyacrylamide SDS gels and Western blotting utilizing a monospecific antibody directed against a synthetic peptide corresponding to residues 526 to 543 of pmHAS (acetyl-LDSDDYLEPDAVELCLKE-amide) as described hereinabove.

[000310] The DNA encoding different segments of pmHAS-D or pmCS were generated by amplifying the pPm7A insert or pPmF4A insert, respectively, by 15 cycles of PCR with Taq polymerase (Fisher) and synthetic oligonucleotide primers corresponding to various portions of the pmHAS-D or pmCS open reading frame. Each internal primer contained overlaps with the other segment to allow joining of the two desired segments. The forward and reverse primers for pmHAS residue 1-427 (A segment) were P1 = 5'-ATGAACACATTATCACAAGCAATAAAAGC-3' (SEQ ID NO:53) and P2 = 5'-GCGAATCTTCTATTGGTAAAAGYTTTC-3' (SEQ ID NO:54) (Y=C/T), respectively. The forward and reverse primers for pmCS residue 421-704 (C segment) were P3 = 5'-CTTTTACCAATAGAAGATTCGCATAT-3' (SEQ ID NO:55) and P4 = 5'-GAAGACGTCTTAGGCATCTTTATTCTGAATGAG-3' (SEQ ID NO:56), respectively. The forward and reverse primers for pmCS residue 1-420 (D segment) were P1 and P2. The forward and reverse primers for pmHAS residue 428-703 (B segment) were P3 and P5 = 5'-GGGAATTCTGCAGTTAAATATCTTTTAAGATATCAATCTCTTC-3' (SEQ ID NO:57), respectively. The chimeric or hybrid synthases were created by 15 cycles of PCR with the gel-purified (GeneClean; Bio101) segments and outer primers (pm-AC used A and C segments with primer P1 and P4; pm-BD used B and D segments with primer P1 and P5). The purified PCR products were cloned into pETBlue-1 vector and the chimeric or hybrid proteins were expressed in Tuner(DE3)pLacI cells (Novagen). The complete open reading frames of multiple clones of both constructs were sequenced. A pmAC construct that was perfect, was found but both of the two

pmBD constructs that we had sequenced completely had secondary undesired mutations (#1, E695 and I697F; #2, I302V). However, these mutations were in different locations and the enzyme transferase activities were identical. Several other pmBD clones have the identical phenotype but their complete sequences were not determined.

[000311] *Analysis of Genomic DNA and Isolation of Capsule Biosynthesis Locus DNA* - Preliminary data from Southern blot analysis using pmHAS-based hybridization probes [12] suggested that the Type A synthase and the putative Type D synthase were not very similar at the DNA level. However, PCR suggested that the UDP-glucose dehydrogenase genes, which encode an enzyme that produces the UDP-GlcUA precursor required for both HA and heparin biosynthesis, were very homologous. In most encapsulated bacteria, the precursor-forming enzymes and the transferases are located in the same operon. To make a hybridization probe predicted to detect the capsule locus, Type D chromosomal DNA served as a template in PCR reactions utilizing degenerate oligonucleotide primers (sense: GARTTYBTIMRIGARGGIAARGCIYTITAYGAY (SEQ ID NO:58); antisense: RCARTAICCICCRTAICCRAAISWXGGRTTRTTRTARTG (SEQ ID NO:59), where I = inosine; R = A or G; S = C or G; W = A or T; Y = C or T) corresponding to a conserved central region in many known UDP-glucose dehydrogenase genes. The ~0.3-kb amplicon was generated using Taq DNA polymerase (Fisher), gel-purified, and labeled with digoxigenin (High Prime system, Boehringer Mannheim).

[000312] A lambda library of *Sau3A* partially digested Type D *P. multocida* P-3881 DNA (~4-9 kb average length insert) was made using the *Bam*HI-cleaved λZap Express™ vector system (Stratagene). The plaque lifts were screened by hybridization (5x SSC, 50°C; 16 hrs) with the digoxigenin-labeled probe using the manufacturer guidelines for colorimetric development. *E. coli* XLI-Blue MRF' was co-infected with the purified, individual positive lambda clones and ExAssist helper phage to yield phagemids. The resulting phagemids were transfected into *E. coli* XLOLR cells to recover the plasmids. Sequence analysis of the plasmids using a variety of custom primers as well as the GPS-1 Genome Priming System (New England Biolabs) revealed a novel open reading frame, which we called pmHS1 (DNA sequence facilities at Oklahoma State University and University of Oklahoma HSC). We amplified and sequenced the ORF from several highly encapsulated isolates (see hereinbelow); very similar sequences were obtained.

[000313] *Expression of Recombinant P. multocida Heparosan Synthase* - The pmHS1 ORF (617 amino acids) was amplified from the various Type D genomic DNA template by 18 cycles of PCR with *Taq* polymerase. For constructing the full-length enzyme, the sense primer (ATGAGCTTATTTAAACGTGCTACTGAGC – SEQ ID NO:58) corresponded to the sequence at the

deduced amino terminus of the ORF and the antisense primer (TTTACTCGTTATAAAAAGATAAACACGGAATAAG – SEQ ID NO:59) encoded the carboxyl terminus including the stop codon. In addition, a truncated version of pmHS1 was produced by PCR with the same sense primer but a different antisense primer (TATATTTACAGCAGTATCATTTTCTAAAGG -- SEQ ID NO:60) to yield a predicted 501-residue protein, DcbF (SEQ ID NO:61) (GenBank Accession Number AAK17905); this variant corresponds to residues 1- 497 of pmHS1 followed by the residues TFRK.

[000314] The HA4 molecule was converted into a fluorescent derivative in two steps. First, reductive amination of HA4 with cyanoborohydride and excess diaminobutane in 0.1 M borate buffer, pH 8.5, was used to make an amino-HA4 derivative that was purified by gel filtration on P2 resin. Second, the amino-HA4 was derivatized with the N-hydroxysuccinimide ester of Oregon green 488 (Molecular Probes) and the Fluor-HA4 was purified by preparative normal-phase thin layer chromatography (silica developed with 2:1:1 n-butanol/acetic acid/water).

[000315] Catalyst preparation and in vitro synthesis. The catalyst, pmHAS1-703 or pmCS1-704, are soluble purified E. coli-derived recombinant protein. The enzyme in the octyl-thioglucoside extracts of the cell paste was purified by chromatography on Toyopearl Red AF resin (Tosoh) using salt elution (50 mM HEPES, pH 7.2, 1 M ethylene glycol with 0 to 1.5 M NaCl gradient in 1 hour). The fractions containing the synthase protein (~90% pure by SDS-PAGE/Coomassie-staining) were concentrated by ultrafiltration and exchanged into reaction buffer (1 M ethylene glycol, 50 mM Tris, pH 7.2). The syntheses in general contained synthase, UDP-GlcNAc, UDP-GlcUA, and 5mM MnCl2 in reaction buffer. Reactions are incubated at 30°C for 6 to 48 hrs.

[000316] Analysis of in vitro synthesized HA. HA are analyzed on agarose gels as described in Lee and Cowman. In brief, agarose gels (0.7-1.2%) in 1x TAE buffer were run at 40V. Gels are stained with Stains-All dye (0.005% w/v in ethanol) overnight and destained with water. HA was analyzed on acrylamide gels (15-20%) as described in Ikegami-Kawai and Takahashi. To purify HA, pmHAS was removed by choloroform extraction and HA are precipitated with three volumes of ethanol and the pellets were redisolved in water. Alternatively, the unincorporated precursor sugars were removed by ultrafiltration with Microcon units (Millipore). The concentration was determined by carbazole assay (ref) and a glucuronic acid standard.

[000317] Gel filtration/multi-angle laser light scattering analysis was used to determine the absolute molecular weights. Polymers were separated on two tandem Toso Biosep TSK-GEL columns (6000PWXL followed by 4000PWXL; each 7.8 mm´30 cm; Japan or equivalent) eluted

in 50 mM sodium phosphate, 150 mM NaCl, pH 7 at 0.5 mL/min. The eluant flowed through an Optilab DSP interferometric refractometer and then a Dawn DSF laser photometer (632.8 nm; Wyatt Technology, Santa Barbara, CA) in the multi-angle mode. The manufacturer's software package was used to determine the absolute average molecular weight using a dn/dC coefficient of 0.153.

[000318] Although the foregoing invention has been described in detail by way of illustration and example for purposes of clarity of understanding, it will be obvious to those skilled in the art that certain changes and modifications may be practiced without departing from the spirit and scope thereof, as described in this specification and as defined in the appended claims below.

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